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OM nucleic - nucleic search, using sw model

Run on: January 20, 2004, 16:14:38 ; Search time 533 Seconds
(without alignments)
9764.571 Million cell updates/sec

Title: US-09-890-811B-9
Perfect score: 1928
Sequence: 1 gcacgagtctcatctt.....tcaaaaaaaaaaaaaaaaaa 1928

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03.*
1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1928	100.0	1928	22	AAD09829 Soybean SPFI-relat
2	437.2	22.7	2008	24	ABX26660 Sunflower WRKY pol
3	355.8	18.5	373	25	ABX19178 Human GDP-mannose
4	342.2	17.7	421	25	ABX22865 Human GDP-mannose
5	312.6	16.2	363	25	ABX19862 Human GDP-mannose
6	308.2	16.0	1539	21	AAC43176 Arabidopsis thalia
7	308.2	16.0	1539	24	ABZ12999 Arabidopsis thalia
8	270.2	14.0	1182	24	ABZ13876 Arabidopsis thalia

9	259.2	13.4	1589	21	AAC40213 Arabidopsis thalia
10	256	13.3	265	25	ABX26660 Human GDP-mannose
11	232.8	12.1	2343	24	ABX59412 Soybean WRKY polyn
12	228.8	11.9	1542	24	ABZ12620 Arabidopsis thalia
13	228.8	11.9	1542	25	ABZ42035 Arabidopsis thalia
14	221.6	11.5	2158	22	AAD09830 Wheat SPFI-related
15	221.4	11.5	1545	24	ABZ14474 Arabidopsis thalia
16	221.4	11.5	1545	25	ABZ42023 Arabidopsis thalia
17	208.2	10.8	1626	24	AAI48565 A thaliana WRKY33
18	187.6	9.7	2086	22	AAD09828 Rice SPFI-related
19	177.8	9.2	1617	24	ABX59408 Sunflower WRKY pol
20	176.6	9.2	2603	24	ABK65157 Arabidopsis cDNA e
21	175.6	9.1	2208	24	ABX59420 Maize WRKY polynuc
22	175.4	9.1	378	21	AAK57119 Pinus radiata tran
23	167	8.7	2215	24	ABK65153 Arabidopsis cDNA e
24	166.4	8.6	1961	22	AAD09827 Rice SPFI-related
25	162.8	8.4	403	25	ABX62630 Arabidopsis thalia
26	161.6	8.4	835	24	ABX98908 Arabidopsis thalia
27	158	8.2	1179	24	ABX59416 Maize WRKY polynuc
28	154.6	8.0	930	21	AAK48843 Arabidopsis thalia
29	154.6	8.0	1065	21	AAK47116 Arabidopsis thalia
30	152.6	7.9	1538	24	ABX59406 Sunflower WRKY pol
31	147	7.6	1536	24	ABX59407 Sunflower WRKY pol
32	141.6	7.3	306	25	ABX85599 Corn ear-derived p
33	139.6	7.2	961	24	ABX59414 Wheat WRKY polynuc
34	130.2	6.8	2043	24	AAI48588 A thaliana WRKY33
35	119.4	6.2	1464	24	ABZ13768 Arabidopsis thalia
36	112.2	5.8	522	24	ABX59411 Soybean WRKY polyn
37	111.4	5.8	624	21	AAK38694 Arabidopsis thalia
38	109	5.7	1136	22	AAD05836 Arabidopsis thalia
39	109	5.7	1136	24	ABK65303 Arabidopsis cDNA e
40	108.2	5.6	444	21	AAK45051 Arabidopsis thalia
41	108.2	5.6	548	21	AAK35279 Arabidopsis thalia
42	108.2	5.6	569	21	AAK48380 Arabidopsis thalia
43	107	5.5	837	22	AAF80410 Nucleotide sequenc
44	107	5.5	837	24	ABK65175 Arabidopsis cDNA e
45	107	5.5	843	21	AAK37750 Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AAD09829	ID AAD09829 standard; cDNA; 1928 BP.
XX	XX
AC	AAD09829;
XX	XX
DT	12-SEP-2001 (first entry)
XX	XX
DE	Soybean SPFI-related transcription factor #5 cDNA.
XX	XX
KW	Soybean; SPFI-related transcription factor; transgenic plant;
KW	genetical mapping; physical mapping; plant breeding; ss.
XX	XX
OS	Glycine max.
XX	XX
PH	Key Location/Qualifiers
FT	CDS 12..1739
FT	/*tag= a
FT	/product= "SPFI-related transcription factor #5"
XX	XX
PN	WO200149840-A2.
XX	XX
PD	12-JUL-2001.
XX	XX
PF	22-DEC-2000; 2000WO-US35310.
XX	XX
PR	04-JAN-2000; 2000US-0174325.
XX	XX
PA	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	XX
PI	Zhu Q, Famodu OO, Rafalski JA;

XX WPI: 2001-441876/47.
 DR P-PSDB; AAE05092.
 XX
 PT Novel isolated SPF-1 related transcription factor polypeptides and
 PT polynucleotides useful for producing transgenic plants -
 XX
 PS Claim 7; Page 52-53; 60pp; English.
 XX
 CC The present sequence is soybean SPFI-related transcription factor #5
 CC cDNA. The SPFI-related transcription factor is useful for transforming a
 CC cell by introducing SPFI-related transcription factor into a cell. It is
 CC also useful for producing a transgenic plant by transforming a plant cell
 CC with SPFI-related transcription factor and regenerating a plant from the
 CC transformed plant cell. It is also useful to create transgenic plants in
 CC which SPFI-related transcription factor DNA is present at higher or lower
 CC levels than normal or in cell types or developmental stages in which they
 CC are not normally found. The SPFI-related transcription factor DNA is
 CC useful to prepare antibodies. It is also used as probes for genetically
 CC and physically mapping the genes that they are a part of, and used as
 CC markers for traits linked to these genes. Such information is useful in
 CC plant breeding in order to develop lines with desired phenotype.
 XX
 SQ Sequence 1928 BP; 591 A; 454 C; 387 G; 496 T; 0 other;

Query Match 100.0%; Score 1928; DB 22; Length 1928;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACGAGTCTCATGGCATCTTCTTCTGGTAGTTTACACCTCTGCAAGTGCACAACTCCT 60
 DB 1 GCACGAGTCTCATGGCATCTTCTTCTGGTAGTTTACACCTCTGCAAGTGCACAACTCCT 60

QY 61 TCACCAACTTCACTTCTCCACACACCCCTTTCATGACCACTTCTTCTGACCTCCTTG 120
 DB 61 TCACCAACTTCACTTCTCCACACACCCCTTTCATGACCACTTCTTCTGACCTCCTTG 120

QY 121 CTTCTCCCTTGGACACAAAGCCACACAGGGTGTGTCTGAGAGAACTGGCTCTG 180
 DB 121 CTTCTCCCTTGGACACAAAGCCACACAGGGTGTGTCTGAGAGAACTGGCTCTG 180

QY 181 GTGTTCCTCAATTCAGTCCACACACCACTTCTCTGCTCTCTCTCCCTCCCATTT 240
 DB 181 GTGTTCCTCAATTCAGTCCACACACCACTTCTCTGCTCTCTCTCCCTCCCATTT 240

QY 241 CTCCTTCTTCTTACTTGTCTATTCCTCTGTTGAGCCCTGCTGAGCTTCTTGACTCGC 300
 DB 241 CTCCTTCTTCTTACTTGTCTATTCCTCTGTTGAGCCCTGCTGAGCTTCTTGACTCGC 300

QY 301 CGGTTCCTTAACTCTTCCAACTTCTGCAATCTCCCAACTGGAGCAATTTGTTGCTC 360
 DB 301 CGGTTCCTTAACTCTTCCAACTTCTGCAATCTCCCAACTGGAGCAATTTGTTGCTC 360

QY 361 AGAGCTTCAATTTGGAAGAGCAGTTTCAGGGGGGAATCAGCAAAATTTGCAAGGAAGAGACA 420
 DB 361 AGAGCTTCAATTTGGAAGAGCAGTTTCAGGGGGGAATCAGCAAAATTTGCAAGGAAGAGACA 420

QY 421 AAGGCTTCTCAAAATTTCTTTTCAAAACCCGATCAGGACTCTCTGTTTCATCCACAGCAA 480
 DB 421 AAGGCTTCTCAAAATTTCTTTTCAAAACCCGATCAGGACTCTCTGTTTCATCCACAGCAA 480

QY 481 CATACCACTCTTCAAAATTTCTTCAAGTTCACAGCAACAGCCATGGATTTTTCAGGAGCCA 540
 DB 481 CATACCACTCTTCAAAATTTCTTCAAGTTCACAGCAACAGCCATGGATTTTTCAGGAGCCA 540

QY 541 CGAAACAGGATAATTTTCTTCAGGAAGGGTATGATGAATACTGAAAACTCTTCTTCCA 600
 DB 541 CGAAACAGGATAATTTTCTTCAGGAAGGGTATGATGAATACTGAAAACTCTTCTTCCA 600

QY 601 TGCAGAGTTTTCCTCTGAGATTGCTAGTGTCCAAACTAAACATAGCAATGGGTTTCAAT 660
 DB 601 TGCAGAGTTTTCCTCTGAGATTGCTAGTGTCCAAACTAAACATAGCAATGGGTTTCAAT 660

QY 661 CCGATTATGGCAATTACCCCCCACAATCTCAGACTTTAAGTAGAAGGTGAGATGGGT 720
 DB 661 CCGATTATGGCAATTACCCCCCACAATCTCAGACTTTAAGTAGAAGGTGAGATGGGT 720

QY 721 ACAATTGGAGGAATAATGGCCAAAAACAAGTGAAGGAAGTGAATAATCAAGAAGTTATT 780
 DB 721 ACAATTGGAGGAATAATGGCCAAAAACAAGTGAAGGAAGTGAATAATCAAGAAGTTATT 780

QY 781 ACAAAATGCACATACCCCAATTCGCCCTTACAAAGAAGGTTTTCAGAGGTCTTTAGATGGAC 840
 DB 781 ACAAAATGCACATACCCCAATTCGCCCTTACAAAGAAGGTTTTCAGAGGTCTTTAGATGGAC 840

QY 841 AAAATTACTGAGATAGTTTATAAGGGTACTCATAACCATCTTAAGCTCAAAATCTAGGA 900
 DB 841 AAAATTACTGAGATAGTTTATAAGGGTACTCATAACCATCTTAAGCTCAAAATCTAGGA 900

QY 901 GAAACTCATCAAACTCTCTTCTTGCATCCCTCATTCCTCAATTCCTCAATTCCTCAAA 960
 DB 901 GAAACTCATCAAACTCTCTTCTTGCATCCCTCATTCCTCAATTCCTCAATTCCTCAAA 960

QY 961 TCCAGATCAATCCTATGTCACACATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1020
 DB 961 TCCAGATCAATCCTATGTCACACATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1020

QY 1021 AAAAATCATCAATATCAATTTGGAGATGATGATTTTGGAGAGATTTCCCAAAAGTGTAAAT 1080
 DB 1021 AAAAATCATCAATATCAATTTGGAGATGATGATTTTGGAGAGATTTCCCAAAAGTGTAAAT 1080

QY 1081 CAGGAGGGGATGAATATGATGAAGATGAACCTGTATGTCGCAAAAGATGGAAGTGAAGT 1140
 DB 1081 CAGGAGGGGATGAATATGATGAAGATGAACCTGTATGTCGCAAAAGATGGAAGTGAAGT 1140

QY 1141 AAAATGAGGTATGTCAGCCCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1200
 DB 1141 AAAATGAGGTATGTCAGCCCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1200

QY 1201 AGACAACCACTGACATTTGATATCTTGTATGATGGCTATAGTGGAGAAATATCGGSCAGA 1260
 DB 1201 AGACAACCACTGACATTTGATATCTTGTATGATGGCTATAGTGGAGAAATATCGGSCAGA 1260

QY 1261 AAGTAGTGAAGGGCAATCCAAATCCAAAGGATTTACTTCAAGTGCACACACCCAGGATGC 1320
 DB 1261 AAGTAGTGAAGGGCAATCCAAATCCAAAGGATTTACTTCAAGTGCACACACCCAGGATGC 1320

QY 1321 CAGTGAAGGAGCAGCTGGAAGAGGCTCAGATGACCTAAGGGCTGTGATCACAACCTTATG 1380
 DB 1321 CAGTGAAGGAGCAGCTGGAAGAGGCTCAGATGACCTAAGGGCTGTGATCACAACCTTATG 1380

QY 1381 AGGGAAGCACAACCACTGATGTTCTGCAAGCCCTGCGAGTGGCAGCCATTTCTGTGAACA 1440
 DB 1381 AGGGAAGCACAACCACTGATGTTCTGCAAGCCCTGCGAGTGGCAGCCATTTCTGTGAACA 1440

QY 1441 GACCAATGCCAAACAAATGTTTCAAAACCAACCACTGCGAGCCTTCCGTAAGGCTCT 1500
 DB 1441 GACCAATGCCAAACAAATGTTTCAAAACCAACCACTGCGAGCCTTCCGTAAGGCTCT 1500

QY 1501 TGCCAGTGAATCCCAAGAGTGAATTTCCCTTCAGAACCAAAAGTCAAGAGCACCACAG 1560
 DB 1501 TGCCAGTGAATCCCAAGAGTGAATTTCCCTTCAGAACCAAAAGTCAAGAGCACCACAG 1560

QY 1561 AAGGGCAATCACCTTTCACCTAGAGATGCTACAAAGTCCAGGAAGTTTGGATTTCTCAG 1620
 DB 1561 AAGGGCAATCACCTTTCACCTAGAGATGCTACAAAGTCCAGGAAGTTTGGATTTCTCAG 1620

QY 1621 GGTGGGAATCAATTCGCAATTTTACGTGAACAGCAGCAACTATCTGCAATGTTTCT 1680
 DB 1621 GGTGGGAATCAATTCGCAATTTTACGTGAACAGCAGCAACTATCTGCAATGTTTCT 1680

QY 1681 CCTCCAGGACCAAGGAGGAGCTAGAGATGATGATGCTTCTGATCTCTACTATGCTGAA 1740
 DB 1681 CCTCCAGGACCAAGGAGGAGCTAGAGATGATGATGCTTCTGATCTCTACTATGCTGAA 1740

QY 1741 GGAATTTTTTTTTTCCCTTTTGGTGGTATGAGTATGGAAGTTTGGAAATTTTGGAAAGTGGGGA 1800

Db 1741 GGAATTTTTCCTTTTTCCTAGTATGGAAGTTTGGAAATTTTGGAAAGTGGGGA 1800
QY 1801 CTAGGATTTTATTCGACAAATTAAGTTTCCATTTCGATTTATTTGGTATTTTGGTTTGG 1860
Db 1801 CTAGGATTTTATTCGACAAATTAAGTTTCCATTTCGATTTATTTGGTATTTTGGTTTGG 1860
QY 1861 TTGTAAATTTTATACAGCCACAGATTTGGTATAGTATATATCTAGTATTTCAAAAAA 1920
Db 1861 TTGTAAATTTTATACAGCCACAGATTTGGTATAGTATATATCTAGTATTTCAAAAAA 1920
QY 1921 AAAAAAA 1928
Db 1921 AAAAAAA 1928

RESULT 2
ABS59405
ID ABS59405 standard; cDNA; 2008 BP.
XX AC ABS59405;
XX DT
XX 05-NOV-2002 (first entry)
XX Sunflower WRKY polynucleotide #1.
XX DE
XX KW WRKY; gene; ss; plant; zinc-finger-type factor; WRKY; SAR; sunflower;
KW SA-dependent structure-activity analysis response; pathogen resistance;
KW maize; wheat; rice; soybean.
XX KW
XX OS Helianthus annuus.
XX SS
XX PN US2002076775-A1.
XX PD 20-JUN-2002.
XX PF 16-MAR-2001; 2001US-0810264.
XX PR 17-MAR-2000; 2000US-190467P.
XX PA (CRAN/) CRANE V C.
PA (FAMO/) FAMODU O.
PA (HUXX/) HU X.
PA (LUGG/) LU G.
PA (ZHAN/) ZHANG L.
XX PI Crane VC, Famodu O, Hu X, Lu G, Zhang L;
XX XX
XX WPI; 2002-582922/62.
XX P-PSDB; ABG76909.
XX New isolated plant-specific zinc-finger-type factor polynucleotide,
XX useful for e.g. regulating the SA-dependent structure-activity analysis
XX response in a plant -
XX Claim 21; Page 32-34; 66pp; English.
XX The invention relates to an isolated polynucleotide encoding a
XX plant-specific zinc-finger-type factor (WRKY) protein. The DNA and
XX protein are used to modulate the level of a WRKY protein in a plant and
XX to regulate the SA-dependent structure-activity analysis (SAR) response
XX in a plant. The sequences can be used to engineer plants to resist
XX pathogens such as viruses, bacteria, insects and fungi, and to survive
XX stress. They may also be used as a molecular probe to track inheritance
XX of corresponding loci in genetic crosses and facilitate the plant
XX breeding process, to isolate, identify and genetically map WRKY and other
XX closely related disease resistance genes and to find genes and their
XX promoters that respond to a WRKY domain. This sequence represents DNA
XX encoding a WRKY polypeptide of the invention.
XX SQ .Sequence 2008 BP; 616 A; 463 C; 388 G; 541 T; 0 other;
Query Match 22.7%; Score 437.2; DB 24; Length 2008;

Best Local Similarity 57.4%; Pred. No. 5.3e-104;
Matches 1000; Conservative 0; Mismatches 673; Indels 69; Gaps 9;
QY 17 ATCTCTCTCTGTTAGTGTGACACCTCTGCAAGTGCACAACTCTCTCACCACTTCACTT 76
Db 23 ATCTCTCTCTATAAGTGTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 82
QY 77 TCTCCACACCCCTTTTCATGACCACTTTCTCTCTGACCTCTCTCTCTCTCTCTCTCTCT 136
Db 83 TCTCCACCCCT 142
QY 137 CAACAAGCCACACAGGTGTTGTTCTGAGAGAACTGGCTCTGGTGTGTTTCCAAATTC 196
Db 143 AACCAACCGGACTCGCTGCGCGGATCGCGAACGAGTCGGCTCGGTATTTCCAAAGTCAA 202
QY 197 GTCCACACCCACCT 256
Db 203 GTCAATCTCTCACT 262
QY 257 TGCTATCTCTCTGTTTGTAGCCCTCTGAGCTTTCTGACTCGCGGTTCTCTCTAACTC 316
Db 263 TGCTATCTCTCTGTTTGTAGCCCTCTGAGCTTTCTGACTCGCGGTTCTCTCTAACTC 322
QY 317 TTCCAAATCTCTGCTATCTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAA 376
Db 323 TTCCAAATCTCTGCTATCTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAA 382
QY 377 GA-----CGAGTTCAAGGGGGAATCAGCAAAATTTGCAAGGAGAGAGACAAAAGCTT 427
Db 383 GAATCTGAACGGCAACTTCCATAATGAAGAACTAGATCAAAAGGAGACAAAAGCTT 442
QY 428 CTCAAAATTTCTCTTTCCAAACCGGATCAGGACTCTCTCTCTCTCTCTCTCTCTCTCT 487
Db 443 GCGGATTTCTCTTTTCGACCACT-----TGCTATCTCTCTAGGAGCAACAGATAT 495
QY 488 GTCTTCAATGTCAAGTTTCAAACTCAAGCAGCAGTGGAGTTTTCAGGAGGCCACGAAACA 547
Db 496 GGAATAATCAGAAACAAACAGATAGATCAGAGCAAAATCTTTTAAACCAATCGGACACT 555
QY 548 GGATAATTTTCTCTCAGGAAAGGGTATGATGAAACTGAAACTCTCTCTCTCTCTCTCT 607
Db 556 CGCC-----TCCGATGAGAGCTTCTCACCGGAAATCGCAAACTTCAAACT----- 601
QY 608 TTTTCTCTCTGAGATTGTCTGATGTCTCAAACTAACCATAGCAATGGGTTTCAATCCGATTA 667
Db 602 -----CGATTCAAACTCACAAGCACAAGCTTCCAACTCTGTT-ATGACACCAA 649
QY 668 TGGCAATTACCCCCCACTCTCAGACTTTTAAGTAGAGGTGAGATGATGGGTACAAATTG 727
Db 650 CAGCAGCAGCAACTTCAACCAACCAACCGTTACAGAAAGTTCAGAAAGCGTTTATAATTG 709
QY 728 GAGGAATATGCGCAAAACAACTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 787
Db 710 GCGAAATATCAGGCGCAAAACAAAGTGAAGGAGCGGAAACCCGAGAGGTTTATACAA 769
QY 788 CACATACCCCAATTCCTCTTCAAAAGAAAGTGTGAGAGGTCTTTAGATGGACAAATTAC 847
Db 770 CAGGTATCAAAATTTCTCAATGAAGAGAACTAGAGACTATATAGAGGACAGATTAC 829
QY 848 TGAGATAGTTTATAGGGTACTCATAAACCATCTTAAGCTCTCAAAATCTAGAGAGAACTC 907
Db 830 TGAGATAGTTTATAGGGTAACTATAATCACCAGAAACCGCAATCTTACGCGAAGATCATC 889
QY 908 ATCAAACT 955
Db 890 GTCT 949
QY 956 TGAATCTCCAGATCAATCTCTATGCGACACATGGAAGTGGACAAATGAGTTTCACTGCTCC 1015
Db 950 TGAATCTCCAGATCAATCTCTATGTTTCTCTATGATGATGCGGAGGTTGATTCGGTTACT 1009
QY 1016 CCCAGAAAACTCATCAATATCAATTTGGAGATGATGATTTTGGAGCAGAGTTTCCCAAGTG 1075

Db 1010 GCCGGAATTCCTTCGATTTTCGTCGAGATGATGATTTGATCGGAGT-----AGGTC 1063
 Qy 1076 TAAATCAGGAGGGATCAATATGATGAGATGACCTGATGCCAAGATGGAATTTGA 1135
 Db 1064 CGGTGGGATGGTGTACTGTTGATGAAGATGAGCTGAGGCCAAGATGGAAGGTGTC 1123
 Qy 1136 AGGTGAATGAGGGTATGTCAGCCCTGGAAGTGAACACAGTGAAGAACCTAGAGTTGT 1195
 Db 1124 GGAATGAAGGATATCAATGATTTGGTGAACAGAGCGGTACGAGACCGAGATCGT 1183
 Qy 1196 AGTTCAGACACAGTACATTCATTCCTTGTATGATGCTATAGTGGAGAAAATACGG 1255
 Db 1184 GGTTCAAACGACGAGATATTCATATCTCGATGATGTTATAGATGGAAGAAATACGG 1243
 Qy 1256 GCAGAAAGTGAAGGGCAATCAATCAAGAGTACTACAAGTGCACACACCCAGG 1315
 Db 1244 TCAAAAGGTGTCAGGGGAAACCAATCCAGAGGTATTATCAAAATGCAACAAGTCTAGG 1303
 Qy 1316 ATGTCAGTCAAGGAGCAGCTGGAAGAGCTCACATGACCTAAGGCTGTGATCAAC 1375
 Db 1304 TTGTTCTGTAAGAAACATGTGAGCGAGCGTCAAGAGCTTGAGGTCAATTAAGAC 1363
 Qy 1376 TTATGAGGAAAGCACCAACCATGATGTTCTGAGCCCGTGGCAGTGGCAGCAATCTGT 1435
 Db 1364 CTACGAGGAAACACCAACCATGATGTCCTCAATGGCTCGTGGTCTG---GCCATCGTT 1420
 Qy 1436 GAACAGACCAATGCCAACAATGCTTCAACACCAACCACTGCAGCCACTTCGGTAAG 1495
 Db 1421 ACAAGCTTCAACCTTAGCAACAATCGCCCTCGATGACAAATTAACCTATGCACTATC 1480
 Qy 1496 GCTCTTCCAGTATCCACCAAGTGAACAATTCCTTCAGAACCAAGATCAACAGCACC 1555
 Db 1481 TCATTATCAAGTTGACAACTCCATGCTGATCAACTCTGTCGCGAGGTACCTCGCTC 1540
 Qy 1556 ACCAGAGGGCAATCACCTTCCACCTAGAGATGCTACAAAGTCCAGGAAGTTTGAT 1615
 Db 1541 ATCTGAAATCAAGCACCTTTTACGTTGGAGATGTTACAAAGTCTGATAATTTAAGTA 1600
 Qy 1616 CTCAGGTTTGGGATCCATGCAATCTTACGTGAGACCAAGCAGCACTATCTGACATGT 1675
 Db 1601 TTCAGATTTGAGATGATGATGAGTCAATTAATGAACATAATTCAGAAAGACGTT 1660
 Qy 1676 TTTCTCTCCAGGACCAAGGAGGCTTAGAGATGACATGTTCTTGGAGTCTCTACTATG 1735
 Db 1661 T-----TCTACGACTAAGAGAACCTAGAGATGACATGTTCTTGGATCACTACTCT 1714
 Qy 1736 CT 1737
 Db 1715 CT 1716

RESULT 3

ID ABX19178 standard; cDNA; 373 BP.
 XX
 AC ABX19178;
 XX
 DT 10-FEB-2003 (first entry)
 XX
 DE Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #1235.
 XX
 KW Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;
 KW cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
 KW arthritis; asthma; sepsis; reperfusion injury; stroke; infection;
 KW complex carbohydrate; gene replacement therapy; immunosuppressive;
 KW antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
 KW antiasthmatic; vasotropic.
 OS Homo sapiens.
 XX
 FN US2002110548-A1.
 XX
 PD 15-AUG-2002.

XX 11-JUN-2001; 2001US-0878574.
 XX 22-NOV-1996; 96US-0753233.
 PR 03-DEC-1997; 97US-0984246.
 PR 09-SEP-1998; 98US-0149674.
 PR 14-JUN-1999; 99US-0333177.
 XX (GEMY) GENETICS INST INC.
 PA
 XX Sullivan F, Kriz R, Kumar R;
 PI WPI; 2003-066673/06.
 XX
 XX New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
 PT peptide, for manufacturing complex carbohydrates, or as targets for
 PT screening GM4,6D antagonists for treating e.g. arthritis, or transplant
 PT rejection -
 XX Disclosure; SEQ ID NO 1237; 6pp; English.
 XX
 XX The invention relates to a composition comprising a human GDP-mannose
 CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
 CC GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation
 CC in a mammalian subject and for treating or ameliorating diseases affected
 CC by the level of cellular fucosylation or diseases affected by the
 CC fucosylation of glycoconjugates. These diseases include arthritis,
 CC transplant rejection, asthma, sepsis, reperfusion injury, stroke or
 CC infection. The GM4,6D peptide or a polynucleotide encoding it is also
 CC useful for manufacturing complex carbohydrates and as targets for
 CC screening small molecule antagonists of the activity of the enzyme. The
 CC polynucleotide is useful in developing an assay for defects in the
 CC enzyme, as well as in gene replacement therapy. Sequences
 CC ABX17942-ABX17944 and ABX17947-ABX17949 represent DNA molecules encoding
 CC human GM4,6D peptides of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 373 BP; 67 A; 131 C; 56 G; 119 T; 0 other;
 Query Match 18.5%; Score 355.8; DB 25; Length 373;
 Best Local Similarity 99.4%; Pred. No. 5.1e-83;
 Matches 357; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GCACGAGTCTCATGGCATCTTCTTCTGGTAGTTAGACACCTCTGCAAGTGCAACTCCT 60
 Db 15 GCTCGAGTCTCATGGCATCTTCTTCTGGTAGTTAGACACCTCTGCAAGTGCAACTCCT 74
 Qy 61 TCACCAACTTTCACCTTCTCCACACACCTTTCATGACCACTTCTTCTCTGACCTCCTTG 120
 Db 75 TCACCAACTTTCACCTTCTCCACACACCTTTCATGACCACTTCTTCTCTGACCTCCTTG 134
 Qy 121 CTTCTCCCTTGGACAAACAAGCCACCAAGCCACAGGGTGGTTGTGTGAGAACTGGGCTCTG 180
 Db 135 CTTCTCCCTTGGACAAACAAGCCACCAAGCCACAGGGTGGTTGTGTGAGAACTGGGCTCTG 194
 Qy 181 GTGTTCCCAAAATTCAGTCCACACCACTTCTCTGCTCTCTCTCCCTCCCAATTT 240
 Db 195 GTGTTCCCAAAATTCAGTCCACACCACTTCTCTGCTCTCTCTCTCCCTCCCAATTT 254
 Qy 241 CTCCTTCTTCTTACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 300
 Db 255 CTCCTTCTTCTTACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 314
 Qy 301 CGGTCTCTCTTAACTCTTCCAAATTCCTCCAACTCTCCAACTCTCCAACTCTCCAACTCT 359
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 RESULT 4
 ID ABX22865
 ID ABX22865 standard; cDNA; 421 BP.

CC polynucleotide is useful in developing an assay for defects in the
 CC enzyme, as well as in gene replacement therapy. Sequences
 CC ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding
 CC human GM4,6D peptides of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 363 BP; 67 A; 128 C; 52 G; 116 T; 0 other;

Query Match 16.2%; Score 312.6; DB 25; Length 363;
 Best Local Similarity 93.7%; Pred. No. 1e-71;
 Matches 340; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

QY 15 GCATCTTCTTCTGGTAGTTAGACACCTCTGCAAGTGCAAACTCCTTCACCAACTTCACC 74
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 DB 1 GCATCTTCTTCTGGTAGTTAGACACCTCTGCAAGTGCAAACTCCTTCACCAACTTCACC 60
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QY 75 TTCTCCACACACCTTTTCATGACACCTTCTTCTGACCTCCTTGTCTTCTCCCTTGGAC 134
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 DB 61 TTCTCCACACACCTTTTCATGACACCTTCTTCTGACCTTCTTGTCTTCTCCACAGAC 120
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QY 135 AACAAAGCCACACACA-----GGTGGTTTGTCTGAGAGAACTGGCTCTGGTGT 185
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 DB 121 AACAAAGCCACACACATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGC 180
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QY 186 CCCAAATTCAGTCCACACACACACCTTCTGCTCTCTCTCCCTCCCATTTCTCCT 245
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 DB 181 CCCAAATTCAGTCCACACACACACCTTCTGCTCTCTCTCCCTCCCATTTCTCCT 240
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QY 246 TCTTCTTACTTGTATCTCTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 305
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 DB 241 TCTTCTTACTTGTATCTCTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 300
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QY 306 CTCCTTAACCTTTCCAACTTTGCTCCATCTCCAACTGAGAGATTTGTTGCTCAGAGC 365
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 DB 301 CTCCTTAACCTTTCCAACTTTGCTCCATCTCCAACTGAGAGATTTGTTGCTCAGAGC 360
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QY 366 TTC 368
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 DB 361 TTC 363

RESULT 6
 AAC43176
 ID AAC43176 standard; DNA; 1539 BP.
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 AC AAC43176;
 XX
 DT 17-OCT-2000 (first entry)
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38308.
 XX
 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
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 OS Arabidopsis thaliana.
 XX
 EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
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Query Match 16.0%; Score 308.2; DB 21; Length 1539;
Best Local Similarity 67.1%; Pred. No. 2.9e-70;
Matches 493; Conservative 0; Mismatches 218; Indels 24; Gaps 3;

QY 710 AGATGATGGGTACAAATGGAGGAAATATGGCCAAATAAGTGAAGGGAAGTGAATAATCC 769
DB 528 AGAGGATGTTACAAATGGAGGAAATATGGCCAAATAAGTGAAGGGAAGTGAATAATCC 587
QY 770 AAGAAGTTATTACAAATGCACATACCCCAATGGCCCTCAAAAGAGAGAGAGTTGAGAGGTC 829
DB 588 TCGGAGTTACTATAAGTGTACTTTCCTTAATGTCCAAAGAGAGAGAGTTGAGAGGATC 647
QY 830 TTATGATGACAAATTAAGTGTATTAAGGTTACTATACCAATCCATCAATCAATCCATCA 889
DB 648 TTGGAAGGTGAGATCAGAGATGTTATTAAGGAGGCAACACCAATCCCTAAACCTCA 707
QY 890 AAATAGTAGGAGAAATCATCAAACTCCTCTCTCTGCAATCCCTCAATCAATCAATCCAT 949
DB 708 GTCTACTAGAGATCTTCTCTCTCTCTGCAATCCCTCAATCAATCAATCCATCAATCCAG 767
QY 950 CAGAACTGAAATCC-----CAGATCAATCCTATGCCACACATGGAGTGGACA 997
DB 768 TTGGATCATTAATCGTCAAGCTTCTCTGATCAGGCTAATTCCTCAATATAGCTTTTCATCA 827
QY 998 AATGGATTCAGCTGCCACCCAGAA-----NACTCAATCAATCAATTCGGAGATGA 1048
DB 828 GTCTGATTCCTTTGGGATGCAACAGAGAGATAACTACTCTCTGATTCCTGTTGGTGACGA 887
QY 1049 TGATTTTCAGCAGAGTTCCCAAAAGTGAATACAGAGGAGTGAATATGATGAAGATCA 1108
DB 888 TGAGTTTCGACAGGCTC---ATCGATTCAGCAGAGACGAGAGAGATTCGGAGTGA 944
QY 1109 ACCTGATGCCAAAGATGGAATTTGAAGGTGAAATGAGGATATGTGAGCCCTCGGAAG 1168
DB 945 ACCTGAACGAAGAGATGGAAGGGAACAATGAAACAAATGGTGGGAATGGTGGTGAAG 1004
QY 1169 TAGAACAGTGAAGAACCTAGAGTTGTAGTTTCAGACCAACAGTGCACATGATCTTTGA 1228
DB 1005 CAAGACAGTGAAGAGCGGAGAAATCGTAGTCAGACCAACGAGTGTATATGACATTCCTGA 1064
QY 1229 TGATGCTATAGTGGAGAAATACGGGCAAGAGTGTAGAGGCAATCCAAATCCCAAG 1288
DB 1065 CGACGGTTACAGATGAGAGAAATACGGGCAAGAGTGTAGAGGAAACCCAAATCCCAAG 1124
QY 1289 GAGTTTACTACAGTGCACACACCCAGGATGTCCTGAGGAGACGCTGGGAAGACCTTC 1348
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Query Match 13.4%; Score 259.2; DB 21; Length 1589;
Best Local Similarity 62.3%; Pred. No. 2.1e-57;

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Qy	683	ACAATCTCAGACATTTAA	GTAAAGGTCAGATGATGGT	TACAAATTTGGAGGAAATATGGCCA	742				
Db	559	ACCAGCATACATGCTGAGTAGGAACTCTAATGATGGTTATG	TTATGGTTGGAGAAATACGGTCA	618					
Qy	743	AAAACAGTGAAGGGAAGTGA	AAATCCAAAGAGTTATTACAAATGCACATACCCCAATTG	802					
Db	619	GAACAAGTGAAGAGGCGAAAA	CCCTAGGAGTTACTTCAAGTGTACGTPATCCTGATTG	678					
Qy	803	CCCTACAAAGAAAGGCTG	CAGAGGTCCTTTAGATGGACAAATTTACTTGAGATAGTTTATAA	862					
Db	679	TGTTTCCAGAGAGATGTTG	AGACGGCTTCTGATGCACAGATCAGTGAGATCAITTTATAA	738					
Qy	863	GGGTACTCATAAACATCCT	TAAGGCTCAAAATATCTAGGAGAAATCTATCAAACTCCTCTTC	922					
Db	739	AGGTGGTCAATAATCATCT	TAAGCTGAGTTTCAACAGAGA-----	778					
Qy	923	TCITGGCAATCCCTCATTC	CAAAATTTCCATCAGAACTGAAATCCCAGATCAATCCCTATGCCAC	982					
Db	779	-----CATCTCAATCTTC	TATTAACCATCATCGGTTAATGGGAGCGCGTTGTTTAATCC--	831					
Qy	983	ACATGGAAGTGGACAAAT	TGATTCAGCTGCCACCCACAGAAAACTCATCAATATCAATTTGG	1042					
Db	832	---TGCTCTGTTGTTAGT	CGAACCTCATGATCAATCAGAGAACTCTTCGATTTGCTTTGA	888					
Qy	1043	AGATGATGATTTTGAGCAG	AGTTTCCCAAAAGTGTAAATCAGAGGGGATGAATATGATGA	1102					
Db	889	CTATAGTGATCTTGAGCAG	AAAAAGTTTAAATCAGAGTATGGTGAGATAGATGAAGAGGA	948					
Qy	1103	AGATGAACCTGATGCCAA	AGATGGAAAAATTTGAAGTGAATAATGAGGGTATGTCAGCCCC	1162					
Db	949	GGAAACAACCTTGAGATGA	AGAGAGATGAAGAGAAAGGTGAAGTGAAGGGGATGCTATAGA	1008					
Qy	1163	TGGAAGTAGAACAGTG-	AGAGAACCTAGAGTTGTAGTTTCAGACAAACAGATGCATTTGATA	1221					
Db	1009	AGTAAGCAAGGAGTTWA	AGAGCCAGAGTTGGTTTCAGACAAATAAGTGAATTTGATG	1068					
Qy	1222	TCCTTGATGATGCTATA	GGTGGAGAAAAATACGGGCAGAAAAGTAGTGAAGGGCAATCCAA	1281					
Db	1069	TTCTTATAGATGGCTTT	TAGATGGAGGAAATATGGTCAAAAAGTTGTCAAAAGGAAATACTA	1128					
Qy	1282	ATCCAGGAGTTTACTACA	AGTGCACACCCAGGATGTCCAGTGAGGAGACATGCGAAA	1341					
Db	1129	ATCCAAGGAGCTACTACA	AGTGCACATTCCAAGGTTGTGGAGTGAAGAACCAAGTGGAAA	1188					
Qy	1342	GAGCCTCACATGACCTTA	AGGGCTGTGATCAAACTTATGAGGGAAGACCAACCATGATG	1401					
Db	1189	GATCCGACGACAGCAG	AGAGCAGTCTCTACTATGAGAGAGACACATCAAGATA	1248					
Qy	1402	TTCTGACGCCCTGGCAG	TGGCAGCCATTTCTGTGAAC	1439					
Db	1249	TCCCAACCGGGCTACG	TGCTCGTGAATTTATTTGGGAC	1286					

RESULT 10
ABX26660

ABX28660
ID ABX26660 standard: cDNA: 265 BP.

[illegible]

AC ABX26660;

XX

DT	11-FEB-2003 (first entry)	Human GDP-mannose 4,6-dehydratase (GM4, 6D) DNA #8717.
XX		
DE		
XX		
XX		Human; GDP-mannose 4,6-dehydratase; GM4, 6D; gene; ss; inflammation;
KW		cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
KW		arthritis; asthma; sepsis; reperfusion injury; stroke; infection;
KW		complex carbohydrate; gene replacement therapy; immunosuppressive;
KW		antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
KW		antidiasthmatic; vasotropic.

OS Homo sapiens.

RESULT 11
ABS59412

ABS59412
ID ABS59412 standard; cDNA; 2343 BP.

XX	US2002110548-A1.
PN	
XX	15-AUG-2002.
XX	
XX	11-JUN-2001; 2001US-0878574.
XX	
PR	22-NOV-1996; 96US-0753233.
PR	03-DEC-1997; 97US-0984246.
PR	09-SEP-1998; 98US-0149674.
PR	14-JUN-1999; 99US-0333177.
XX	
PA	(GEMY) GENETICS INST INC.
XX	
PI	Sullivan F, Kriz R, Kumar R;
XX	
XX	WPI; 2003-066673/06.
XX	
PT	New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
PT	peptide, for manufacturing complex carbohydrates, or as targets for
PT	screening GM4,6D antagonists for treating e.g. arthritis, or transplant
PT	rejection -
XX	
PS	Disclosure: SEQ ID NO 8719; 6pp; English.

Query Match 13.3%; Score 256; DB 25; Length 265;

Best Local Similarity 98.1%; Pred. No. 6.1e-57;

Matches 259; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OV 510 ACACAA CAGCCATGGAGTTTTCAGGAGGCCACGAAACAGGATAATTTTTCCTCAGGAAAG 569

100

DD 2 ACACAAACAGCCATGGAGTCTTCAGGAGGCCACGGAATAACTTCTTCAGGAAATAG GT

570 GGTATGATGA^{AA}AACTCTTCTTCCATGCAGAGT^{TTT}TCCCTGAGATTGCTAGT 629

db 62 GGTATGATGAAACTGAAACCTCTTCTTCCATGCAGAGTTTTCCTGAGATTGCTAGT 121

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QY GTCATTAACCAIAGCAATGGTTCATTCGATTAATGGCAATATACCCCCACAACTC 689

Db
122 GTCCAAACTAACCATAGCAATGGGTTTCAATCCGATCATGGCACTTACCCCCACAATCT 181

690 CAGACCTTTAAGTAGAAGGTCAGATGATG

QY CAGACIITAGTAGTGGTCAGATGATG
039

UD5 182 CAGACTTTAAAGTAGAAGGTCAGATGATGGGTACAAATGGAGGAAATATGGTCAAAACCCA 241

GTGAAGGGAAGTGAAAAATCCAAGA 773

XX AC ABS59412;
 XX DT 05-NOV-2002 (first entry)
 XX DE Soybean WRKY polynucleotide #2.
 XX KW WRKY; gene; ss; plant; zinc-finger-type factor; WRKY; SAR; sunflower;
 KW SA-dependent structure-activity analysis response; pathogen resistance;
 KW maize; wheat; rice; soybean.
 XX OS Glycine max.
 XX PN US2002076775-A1.
 XX PD 20-JUN-2002.
 XX PF 16-MAR-2001; 2001US-0810264.
 XX PR 17-MAR-2000; 2000US-190467P.
 XX (CRAN/) CRANE V C.
 XX (FAMO/) FAMODU O.
 XX (HUX/) HU X.
 XX (LUGG/) LU G.
 XX (ZHAN/) ZHANG L.
 XX Crane VC, Famodu O, Hu X, Lu G, Zhang L;
 PI WPI; 2002-582922/62.
 DR P-PSDB; ABG76916.
 XX New isolated plant-specific zinc-finger-type factor polynucleotide,
 PT useful for e.g. regulating the SA-dependent structure-activity analysis
 PT response in a plant
 XX Claim 21; Page 47-48; 66pp; English.
 XX The invention relates to an isolated polynucleotide encoding a
 CC plant-specific zinc-finger-type factor (WRKY) protein. The DNA and
 CC protein are used to modulate the level of a WRKY protein in a plant and
 CC to regulate the SA-dependent structure-activity analysis (SAR) response
 CC in a plant. The sequences can be used to engineer plants to resist
 CC pathogens such as viruses, bacteria, insects and fungi, and to survive
 CC stress. They may also be used as a molecular probe to track inheritance
 CC of corresponding loci in genetic crosses and facilitate the plant
 CC breeding process, to isolate, identify and genetically map WRKY and other
 CC closely related disease resistance genes and to find genes and their
 CC promoters that respond to a WRKY domain. This sequence represents DNA
 CC encoding a WRKY polypeptide of the invention.
 XX SQ Sequence 2343 BP; 717 A; 527 C; 482 G; 617 T; 0 other;
 Query Match 12.1%; Score 232.8; DB 24; Length 2343;
 Best Local Similarity 59.5%; Pred. No. 2e-50;
 Matches 437; Conservative 0; Mismatches 282; Indels 15; Gaps 2;
 QY 703 GAAGGTGAGTGGGTACAAATGGAGGAAATATGGCCAAAACAAAGTGAAGGAGTG 762
 DB 867 GAGTATCTGATGGATACAACTGGAGAAATATGGCCAAAACAAATGTTAAAGGAAGTG 926
 QY 763 AAAATCAAGAGTTATTACAAATGCAATCCCAATGGCCCTACAAAGAGAGTTG 822
 DB 927 AATTTCCACGCGATTATTACAAATGTACATCTCTGTAAGTTTAAGAAACTATTTG 986
 QY 823 AGAGGTCTTTAGTGGCAATTTACTGAGATGTTTATAGGGTACTCATCAACCATCTTA 882
 DB 987 AACGCTCCCATGATGGCAAAATCACTGAGATAATTTACAGGGAACACATGATCATCTTA 1046
 QY 883 AGCCTCAAAATPACTAGGAGAACTCATCAAACTCTCTCTCTCTCTCAATCCCTCATTTCAA 942
 DB 1047 AACCTCAACGAACCGCGTTACTCTGCGAGAACTAATATGCTGTGCAAGAGACAGAT 1106

QY 943 ATTCATCAGAACTGAAATCCAGATCAATCCTATGCCACATGGAAGTGCACAAATG- 1001
 DB 1107 CTGATAAGCTTCTTTGACTAGCCGAGATGACAAAGGATCCAAATATGTGTGCCAGGGGT 1166
 QY 1002 -----GATTCAGCTGCCACCCAGAAAACATCATCAATATCAATTGGAGATG 1050
 DB 1167 CTCACCTGGCTGAGCCCGGTAACACAGAGTTATTGCTCTGTAGCAAAATGATGGTG 1226
 QY 1051 ATTTTGGACAGAGTTCCCAAAAGTGAATCAGGAGGGGATGAATATGATGAAGATGAAC 1110
 DB 1227 ATCTAGATGTTGGGGGTTTGTCAACCGGAATATGATGAGGTTGATGATGATGATC 1286
 QY 1111 CTGATGCCAAAAGATGGAATTTGAAGGTGAAAATGAGGGTATGTCAGCCCCCTGGAAGTA 1170
 DB 1287 CTTTCTCAAGCGAAGAAAATGGACGTTTGAATTTGCTGACAT---CACTCTGTAGTTA 1343
 QY 1171 GAACAGTGAAGAACCTAGAGTTGTAGTTTCAGACAAACCGTGCACATGATGATCTCTTGATG 1230
 DB 1344 AGCCTATCCGGGAGCCACGTTGTTGTACAAACTCTGAGTGAGGTTGATATCTTTGGATG 1403
 QY 1231 ATGGCTATAGGTGGAGAAATACGGGCGAGAAATAGTAGTGAAGGGCAATCCAAATCCAAGGA 1290
 DB 1404 ATGGCTATCTGCGGCAAGTATGGCGAAGAGTGTGTAGAGGCAATCCTAACCTTAGGA 1463
 QY 1291 GTTACTACAAAGTGCACACACCCAGGATGTCCAGTGAGGAAAGCACTGGAAAGAGCCTCAC 1350
 DB 1464 GTTATTACAAATGCAGAACACCGGTTGCCCGTTAGAAAAACACGTGGAGAGGGCATCTC 1523
 QY 1351 ATGACCTAAGGGCTGTGATCACAATTTATGAGGAAAGCACAAACCATGATGTTCTTGGCAG 1410
 DB 1524 ATGATCCAAAAGCTGTGATTACCATGATGAGGGGAAACACAAATCATGATGTACCAACTG 1583
 QY 1411 CCCGTGGCAGTGGC 1424
 DB 1584 CAAGGAATAGTTGC 1597

RESULT 12

ABZ12620
 ID ABZ12620 standard; DNA; 1542 BP.
 XX AC ABZ12620;
 XX DT 21-JAN-2003 (first entry)
 XX Arabidopsis thaliana stress regulated gene SEQ ID NO 425.
 DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 KW Arabidopsis thaliana.
 XX Arabidopsis thaliana.
 XX WO200216655-A2.
 XX 28-FEB-2002.
 XX 24-AUG-2001; 2001WO-US26685.
 XX 24-AUG-2000; 2000US-227866P.
 PR 26-JAN-2001; 2001US-264647P.
 PR 22-JUN-2001; 2001US-300111P.
 XX (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Harper JF, Kreps J, Wang X, Zhu T;
 PI WPI; 2002-304127/34.
 XX Identifying a stress condition to which a plant cell has been exposed
 PT and producing plants with increased tolerance to these abiotic stresses
 PT
 XX Claim 144; SEQ ID NO 425; 577pp + Sequence Listing; English.
 PS

XX The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:
CC (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and
CC (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.
CC Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.

XX Sequence 1542 BP; 478 A; 332 C; 365 G; 367 T; 0 other;

Query Match 11.9%; Score 228.8; DB 24; Length 1542;
Best Local Similarity 58.9%; Pred. No. 1.9e-49;
Matches 442; Conservative 0; Mismatches 287; Indels 21; Gaps 2;

QY 682 CACAATCTCAGACTTTAAGTAGAGGCTCAGATGATGGTACATTCGAGGAATATGGCC 741
DB 719 CACAGCCTCAAAATGCTGCAAAACAGCTGATGATGATGATGATGATGATGATGATG 778
QY 742 AAAAAACAAGTGAAGGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 801
DB 779 AGAAGCAAGTGAAGGAGGAGGATTTCTCGAGTATTACAAATGATGATGATGATGATG 838
QY 802 GCCCTCAAAAGAAGGTTGAGAGGCTTTTATAGTGAACAAATTTACTGAGATGTTTATA 861
DB 839 GTCTCTGCAAGAAAGTGAAGGAGGCTCACTGATGCAAGTGAAGTGAAGTGAAGTGA 898
QY 862 AGGTTACTATACCATCTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 921
DB 899 AGGTTCAACCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 958
QY 922 CTCTTCAATCCCTCATTCATCAATTCATCAATTCATCAATTCATCAATTCATCAATTC 981
DB 959 GTTCTGATATTGAATCAGTTTCAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1018
QY 982 CACATGGAAGTGACAAATGGAATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT 1041
DB 1019 ACCAGGAACAAGCCCA-----AGTTACAACAACAGAGCAGATGTCGAAGCAAGTG 1069
QY 1042 GAGATCATGATTTTGAAGCAGAGTTCCTCAAAAGTGAAGTGAAGTGAAGTGAAGTGA 1101
DB 1070 ATAGCGAGGAGGTTGGG-----AATGCAAGAGTACTAGTGTGGGGAAGACATG 1117
QY 1102 AAGATCAACTGATGCAAAAGATGGAATTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1161
DB 1118 AGATGAGCTGATCCAGCGAGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1177
QY 1162 CTGGAAGTAGAAGCAGTGAGAGACCTTAGAGTTGATGTTAGTTCAGACAACAGTGAATGATA 1221
DB 1178 CATCGCATAGAAGTGACAGAGCCTTAGGATTTCTCCAAAGCAGAGTGAAGTGAAGTGA 1237
QY 1222 TCCTTGATGATGCTATAGTGTGAGAAATACCGGCGAGAAAGTAGTGAAGGCAATCCAA 1281
DB 1238 TCTTAGATGATGATATAGTGTGCGCAAGTATGTTGTCAGAAAGTAGTCAAAAGGAAAT 1297
QY 1282 ATCCAGGAGTTACTACAAGTGCACACCCAGGATGTCAGTGAAGGAGCAGTGGAA 1341
DB 1298 ATCCGAGGAGCTACTATAAGTGTACAAACAGATTCGCGAGTGAAGGAACATGTAGAGA 1357
QY 1342 GAGCCTTCACATGACCTTAAGGCTGTGATCACAATTTATGAGGAAGACCAACCATGATG 1401
DB 1358 GAGCAGCAACTGACCAAAAGCTGTTGTACACATATGAGGTAAACATACCATGATG 1417
QY 1402 TTCTCTGAGCCCGTGGCAGTGGCAGCCATT 1431
DB 1418 TTCCAGCTGCTAGAACACGAGCAGCCATCAGT 1447

RESULT 13

ABZ42035
ID ABZ42035 standard; cDNA; 1542 BP.
XX
AC ABZ42035;
XX
DT 27-FEB-2003 (first entry)
XX
DE Arabidopsis thaliana gene #19 modulated by PTGS.
XX
KW Posttranscriptional gene silencing; PTGS; plant; transformation; gene;
KW ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 1..1542
FT /*tag= a
XX
PN WO200281695-A2.
XX
PD 17-OCT-2002.
XX
PF 05-APR-2002; 2002WO-EP03806.
XX
PR 06-APR-2001; 2001US-282049P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (FRIE-) FRIEDRICH MIESCHER INST.
XX
PI Zhu T, Glazov EA, Meins F, Wang X, Chang H;
XX
DR WPI; 2003-103337/09.
DR P-PSDB; ABP81191.
XX
PT Novel polynucleic acid segment useful for modulating gene expression within a cell by posttranscriptional gene silencing, and for augmenting a plant cell genome -
PT
PS Claim 18; Page 191-192; 438pp; English.
XX
CC The invention relates to a novel isolated polynucleic acid segment modulated within a cell by posttranscriptional gene silencing (PTGS). The invention specifically relates to a method to identify an expression product that is modulated by PTGS. The polynucleotide is useful for modulating the gene expression within a cell by PTGS, by introducing the polynucleic acid into a cell and expressing the nucleic acid segment in the cell to form a product. The polynucleic acid segment is also useful for augmenting a cell genome, and for augmenting a plant genome, by contacting a plant cell with the segment to produce a transformed plant cell, and growing the transformed plant cell to produce a differentiated transformed plant. The sequences shown in ABZ42017 - ABZ42142 represent segments of A. thaliana cDNA modulated by PTGS.
XX
SQ Sequence 1542 BP; 478 A; 332 C; 365 G; 367 T; 0 other;

Query Match 11.9%; Score 228.8; DB 25; Length 1542;
Best Local Similarity 58.9%; Pred. No. 1.9e-49;
Matches 442; Conservative 0; Mismatches 287; Indels 21; Gaps 2;

QY 682 CACAATCTCAGACTTTAAGTAGAGGCTCAGATGATGGTACATTCGAGGAATATGGCC 741
DB 719 CACAGCCTCAAAATGCTGCAAAACAGCTGATGATGATGATGATGATGATGATGATG 778
QY 742 AAAAAACAAGTGAAGGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 801
DB 779 AGAAGCAAGTGAAGGAGGAGGATTTCTCGAGTATTACAAATGATGATGATGATGATG 838
QY 802 GCCCTCAAAAGAAGGTTGAGAGGCTTTTATAGTGAACAAATTTACTGAGATGTTTATA 861
DB 839 GTCTCTGCAAGAAAGTGAAGGAGGCTCACTGATGCAAGTGAAGTGAAGTGAAGTGA 898

QY 862 AGGTACTCATACCATCTTACGCTCAAAATCTAGGAGAACTCATCAAACTCCTCT 921
 DB 899 AGGTCAACCAATCATGAGCTTCTCAAAAGCGCGTAACTAAGCGGAGTTGAAAA 958
 QY 922 CTCTGCAATCCCTCATCAAAATCTCAAAATCTAGGAGAACTCATCAAACTCCTCT 981
 DB 959 GTTCTGATATGCAATCAGTTTCAAAAGTAAATAGCAGTCTCAAAAGTAAAGAGG 1018
 QY 982 CACATGGAAGTGAACAAATGATTCAGTCCCAACCCAGAGAACTCATCAATCAATTTG 1041
 DB 1019 ACCAGGAAACAAGCCA-----AGTTACAACAACAGAGCAGATGTTGAAGCAAGTG 1069
 QY 1042 GAGATGATGATTTGAGCAGAGTTCCCAAAAGTAAATCAGAGGAGTGAATATGATG 1101
 DB 1070 ATAGCAGGAGGTTGGG-----AATCAGAGACTAGTGTGGGAGAAAGACATG 1117
 QY 1102 AAGATGAACCTGATGCCAAAGATGGAATAATGAAGTGAATAATGAGGGTATGTCAGCCC 1161
 DB 1118 AGGATGAGCTGATCCNAGCGAAGAAATACAGAGTTCCGGGTTTCAGAACCAAGTTGCTT 1177
 QY 1162 CTGGAAGTAGAACAGTGAGAGAACCTGAGTTGATGTTGATGTTGATGTTGATGTTGATA 1221
 DB 1178 CATCGCATAGAACTGTGACAGAGCTAGGATTTATGTTCAAAAGCAGAGTGAAGTTGACC 1237
 QY 1222 TCCTTGTGATGCTATAGTGGAGAAATACCGGAGAGAAAGTAGTGAAGGCAATCCAA 1281
 DB 1238 TCTTAGATGATGATATAGTGGCGCAAGTATGTCAGAAAGTAGTCAAAAGGAAATCCTT 1297
 QY 1282 ATCAAGGAGTGTACTACAGTGCACACACCCAGGATGTCAGTGAGGAGACAGTGGAAA 1341
 DB 1298 ATCCGAGGACTTACTATAGTTTACACACACAGATTCGGAGTAAAGAAACATGTAGAGA 1357
 QY 1342 GAGCCTCACATGACCTAAGGCTGTGATGATCACTATGAGGAGAAAGCAACCATGATG 1401
 DB 1358 GAGCAGCAACTGACCCAAAAGCTGTTGTAACAACATATGAAGTAAACATAACCATGATG 1417
 QY 1402 TTCTCGAGCCCGTGGCAGTGGCAGCAATT 1431
 DB 1418 TTCAGCTGTAGAACCCAGCAGCCATCAGT 1447

RESULT 14

AAD09830
 ID AAD09830 standard; cdna; 2158 BP.

AC AAD09830;

DT 12-SEP-2001 (first entry)

XX Wheat SPFI-related transcription factor #6 cDNA.

XX Wheat; SPFI-related transcription factor; transgenic plant;
 KW genetical mapping; physical mapping; plant breeding; ss.

XX Triticum aestivum.

OS Key Location/Qualifiers
 PH 3..1862
 FT CDS /*tag= a
 FT /product= "SPFI-related transcription factor #6"
 FT /note= "CDS does not include start codon"
 FT /partial

XX WO200149840-A2.

XX 12-JUL-2001.

XX 22-DEC-2000; 2000WO-US35310.

XX 04-JAN-2000; 2000US-0174325.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Zhu Q, Famodu OO, Rafalski JA;
 PI WPI; 2001-441876/47.
 DR P-PSDB; AAE05093.
 XX Novel isolated SPF-1 related transcription factor polypeptides and
 PT polynucleotides useful for producing transgenic plants -
 XX Claim 7; Page 55-56; 60pp; English.
 CC The present sequence is wheat SPFI-related transcription factor #6 cDNA.
 CC The SPFI-related transcription factor is useful for transforming a cell
 CC by introducing SPFI-related transcription factor into a cell. It is also
 CC useful for producing a transgenic plant by transforming a plant cell with
 CC SPFI-related transcription factor and regenerating a plant from the
 CC transformed plant cell. It is also useful to create transgenic plants in
 CC which SPFI-related transcription factor DNA is present at higher or lower
 CC levels than normal or in cell types or developmental stages in which they
 CC are not normally found. The SPFI-related transcription factor DNA is
 CC useful to prepare antibodies. It is also used as probes for genetically
 CC and physically mapping the genes that they are a part of, and used as
 CC markers for traits linked to these genes. Such information is useful in
 CC plant breeding in order to develop lines with desired phenotype.
 XX SQ Sequence 2158 BP; 596 A; 523 C; 549 G; 490 T; 0 other;

Query Match 11.5%; Score 221.6; DB 22; Length 2158;
 Best Local Similarity 60.1%; Pred. No. 1.7e-47;
 Matches 428; Conservative 0; Mismatches 269; Indels 15; Gaps 3;

QY 709 CAGATGATGGTACAAATTCGAGGAAATATGGCAAAACAAAGTGAAGGGAAGTGAATTC 768
 DB 706 CAGATGATGGTACAAATTCGAGGAAATATGGCAAAACAAAGTGAAGGGAAGTGAATTC 765
 QY 769 CAAGAAGTTATTACAATGCACATACCCCAATTCGCCCTACAAGAAAGAGTGGAGGTT 828
 DB 766 CTAGAAGTTATTACAAGTGCACATCCTTAATTTGAAGTAAAAAAGCTATTGGAGCGTG 825
 QY 829 CTTTAGATGACAAATTAAGTATGTTTAAAGGTTACTATACCATCCTTAAGCCCTC 888
 DB 826 CGGTTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 885
 QY 889 AAAATCTAGGAGAACTCATCAAACTCCTCTCTCTGCAATCCTCTCATTTCAATTTCCA 948
 DB 886 AGCTTAATAGGAGTTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 945
 QY 949 TCAGAACTGAAATCCAGATCAATCCTATGCCACACATGGAAG-----TGGACAAA 999
 DB 946 ATGGTGGCGAGCTGCTGATGATAAATCTTCCAATGCTCTTAGCAACCTTGTCTAATCCGG 1005
 QY 1000 TGGATTGAGTGGCCACCCAGAGAACTCATCAATATCAATTTGAGATGATGATTTTGAGC 1059
 DB 1006 TAAATTCGCTGGCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1065
 QY 1060 AGAGTTCCCAAAAGTCTAAATCAGGAGGAGTGAATATGATGAAGATGAACCTGATGCCA 1119
 DB 1066 CTGAGGTGGAAGACCCCTACCTGGGGATGATGCTACAGAGGAGGATTTA---GAGTCGA 1122
 QY 1120 AAAGATGGAATTTGAAGGTGAAATAGGGGTATGTGAGCCCTGGAAAGTAGAACAGTGA 1179
 DB 1123 AACGCAGGAAATGGAGTCTGAGGTATTGAT---GCTGCTCTGATGGGTAAACCTAAACC 1179
 QY 1180 GAGAACTGAGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 1239
 DB 1180 GTGAGCCCGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1239
 QY 1240 GGTGGAGAAATACGGGAGAAAGTAGTGAAGGCAATCCAAATCCAAGAGTTACTTACA 1299
 DB 1240 GTTGGGGAATATGACAGAAAGTTGTCAAGGAAACCCCAATCCACGAGTTACTTACA 1299
 QY 1300 AGTGACACACCCAGGATGTCCAGTGAAGGACCGTGGAAAGAGGCTCATGAGCCTAA 1359

Db 1300 AATGCACAAAGCAGAGATCCCTGTGAGGAAGCATGTTGAGAGAGCATGCGCAGATCCCTA 1359
Qy 1360 GGGCTGTGATCAACATTTATGAGGGAAGACACAAACCATGATGTTCTGTGAGC 1411
Db 1360 ATCAGTGATACACAGGTATGAGGAAACATACCATGATGATGCTGCTGC 1411

RESULT 15

ABZ14474
ID ABZ14474 standard; DNA; 1545 BP.

XX ABZ14474;

XX 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2279.

XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX Arabidopsis thaliana.

XX WO200216655-A2.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US26685.

XX 24-AUG-2000; 2000US-227866P.

XX 26-JAN-2001; 2001US-264647P.

XX 22-JUN-2001; 2001US-300111P.

XX (SCRI) SCRIPPS RES INST.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

XX Identifying a stress condition to which a plant cell has been exposed
XX and producing plants with increased tolerance to these abiotic stresses
XX -

XX Claim 144; SEQ ID NO 2279; 577bp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant
XX cell has been exposed, comprising:
XX (a) contacting nucleic acid representative of expressed polynucleotides
XX in the plant cell with an array or probes representative of the plant
XX cell genome; and
XX (b) detecting a profile of expressed polynucleotides in the plant cell
XX characteristic of a stress response. The method is useful in the
XX production of transgenic plants, cells and seeds and in producing plants
XX with increased tolerance to abiotic stress. The present sequence is that
XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
XX in methods of the invention.
XX CC Note: The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied to Derwent by
XX the European Patent Office.

XX SQ Sequence 1545 BP; 472 A; 356 C; 365 G; 352 T; 0 other;

Query Match 11.5%; Score 221.4; DB 24; Length 1545;
Best Local Similarity 59.0%; Pred. No. 1.6e-47;
Matches 447; Conservative 0; Mismatches 286; Indels 24; Gaps 3;

Qy 679 CCCACAAATCTCAGACTTTTAAGTAGAAGGTTCAGATGATGGGTACAAATTCGAGGAATATG 738

Db 653 CACAACAGCTCTAAATGTTGACAAACCAGCTGATGCTATTAATCTGCGAAATATG 712

Qy 739 GCCAAAAACAAGTGAAGGGAAGTGAATAATCCAAAGAGTTATTACAAATCCATACCCCA 798

Db 713 GGCAAAAGCAAGTAAAGGTAGCGAGTTTCCACGAAGCTATTACAAAGTGTACTTAATCCAG 772

Qy 799 ATTGCCCTTCAAAGAAGGTTGAGAGGTCTTTAGATGGACAAATTAATCTAGAGATAGTTT 858
Db 773 GATGCTCTGTCAAGAAGGTTGAGAGATCTTTGATGGACAAATTAACGGAGATTATCT 832
Qy 859 ATAGGGTACTCATTAACCATCTTAAGCCTCAAAATACTAGGAGAACTCATCAAACTCCT 918
Db 833 ACAAGGTCAGACAAATCAATCACTCTCTCAAAACACTTAAGCGAGGTAAACAAAGATAACA 892
Qy 919 CTTCCTCTTGCATCCCTCAATCAA-----ATTCATCAGAACTGAAT 961
Db 893 CCGCAATATAATGGGAGTTTCGATAAATAACAATCGCGGGAGTTCTGAATTTGGGGCAT 952
Qy 962 CCCAGATCAATCCCTA-----TGGCACAATGGAAGTGGACAAATGGAATCAGCTGCCACCC 1017
Db 953 CACAGTTTCAAACTAATAGCTCCAAAGACTAAGAGAGAGCAACATGAAGCAGTAAGTC 1012
Qy 1018 CAGAAACTCATCAATATCAATTGGAGATGATGATTTTGGAGCAGAGTTCCCAAAAGTGA 1077
Db 1013 AAGCTACGACAAACAGAGCACTTGTCTGAGGCAAGTGACGGTGAAGAAGTTGGTAATGGAG 1072
Qy 1078 AATCAGGAGGGGATGAATATGATGAAGATGAACCTGTGATGCCAAAGATGGAAATTTGAAG 1137
Db 1073 AAACCTGATGTGAGAGAGAAAGATGAGATGAGCTGTATCCCAAGAGAAAGTACAGAAG 1132
Qy 1138 GTGAAAT---GAGGGTATGTCAGCCCTCGAAAGTAGAACAGTAGAGAGAACTTAGAGTTG 1194
Db 1133 TTGGGATTTCAAGAACCACTCTGCTCTTCAATAGAACTGTGACAGAGCCTAGAAATTA 1192
Qy 1195 TAGTTTCAGACACCACTGACATGATATCTTGTATGATGGCTATAGGTGGAGAAATACG 1254
Db 1193 TTGTCCAAACGACGAGTGAAGTTGATCTTCTAGATGATGATATAGGTGGCGGTAAATATG 1252
Qy 1255 GGCAGAAAGTAGTGAAGGGCAATCCAAATCCAAAGGAGTTACTACAAGTGCACACACCCAG 1314
Db 1253 GACAGAAAGTTGTCAAAGGGAATCTTATCCGAGGAGCTACTACAAGTGCACACACCCAG 1312
Qy 1315 GATGTCCAGTAGGGAAGCAGCGTGGAAAGAGCTCTCATGACCTAAGGGCTGTGATCACAA 1374
Db 1313 GATGTGGTGTGAGGAAACATGTAGAGAGAGCAGCAACAGATCCAAAGCTGTAGTAACAA 1372
Qy 1375 CTTATGAGGGGAAGCACAACCATGATGTTCTCGCAGC 1411
Db 1373 CATATGAAGGAAACATAACCATGACCTTCCGCTGC 1409

Search completed: January 20, 2004, 16:25:53

Job time : 538 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2004, 16:14:38 ; Search time 121 Seconds
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Title: US-09-890-811B-9
Perfect score: 1928
Sequence: 1 gcacgagtcctatgcctct.....tcaaaaaaaaaaaaaaaaaa 1928

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	141.6	7.3	306	4	US-09-313-294A-4059
2	80.6	4.2	7218	1	US-08-232-463-14
3	72.2	3.7	7218	1	US-08-232-463-14
4	52.6	2.7	289	3	US-09-007-005-17
5	52.6	2.7	289	3	US-09-244-796-17
6	45	2.3	1105	4	US-09-072-596-329
7	43.8	2.3	1893	4	US-09-328-352-112
8	40.6	2.1	1664976	4	US-08-916-421B-1
9	39	2.0	51259	3	US-08-781-891-209
10	39	2.0	51259	3	US-09-618-166-209
11	39	2.0	1664976	4	US-08-916-421B-1
12	38.6	2.0	275	4	US-08-585-593A-42
13	38.6	2.0	16442	3	US-08-781-891-208
14	38.6	2.0	16442	4	US-09-618-166-208
15	38	2.0	546	4	US-09-134-001C-55
16	38	2.0	1230	4	US-09-461-325-80
17	37.6	2.0	1926	4	US-09-249-585A-2
18	37.6	2.0	1926	4	US-09-410-399-3
19	37.6	2.0	2580	3	US-09-050-863-2
20	37.6	2.0	2580	4	US-09-359-081-2
21	37.6	2.0	5452	2	US-09-130-114-1
22	37.6	2.0	8705	4	US-09-647-344A-14
23	37.6	2.0	9600	3	US-08-910-647-1
24	37.6	2.0	9600	4	US-09-620-925-1
25	37.6	2.0	10596	1	US-07-884-811-15
26	37.6	2.0	10596	1	US-07-885-971-15
27	37.6	2.0	10596	1	US-08-087-783A-15

c 28	37.6	2.0	10596	1	US-08-194-088B-15	Sequence 15, Appl
c 29	37.6	2.0	10596	2	US-08-194-087-15	Sequence 15, Appl
c 30	37.6	2.0	10596	5	PCT-US93-04648-15	Sequence 15, Appl
c 31	37.2	1.9	1656	3	US-09-072-384-14	Sequence 14, Appl
c 32	37.2	1.9	1679	3	US-09-072-384-17	Sequence 17, Appl
c 33	36.6	1.9	248	3	US-09-007-005-32	Sequence 32, Appl
c 34	36.6	1.9	248	3	US-09-244-796-32	Sequence 32, Appl
c 35	36.6	1.9	277	3	US-09-007-005-3	Sequence 3, Appl
c 36	36.6	1.9	277	3	US-09-244-796-3	Sequence 3, Appl
c 37	36.6	1.9	12752	2	US-08-459-146-1	Sequence 1, Appl
c 38	36.6	1.9	12752	2	US-08-459-065-1	Sequence 1, Appl
c 39	36.4	1.9	2007	3	US-08-747-221B-36	Sequence 36, Appl
c 40	36.4	1.9	2007	3	US-08-747-221B-36	Sequence 36, Appl
c 41	36.4	1.9	2007	3	US-09-005-051-38	Sequence 38, Appl
c 42	36.4	1.9	2007	3	US-09-005-051-38	Sequence 38, Appl
c 43	36.2	1.9	1522	4	US-09-615-192A-371	Sequence 371, App
c 44	36.2	1.9	1830121	4	US-09-557-884-1	Sequence 1, Appl
c 45	36.2	1.9	1830121	4	US-09-643-990A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-313-294A-4059
; Sequence 4059, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4059
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700347613H1
US-09-313-294A-4059

Query Match	7.3%	Score 141.6;	DB 4;	Length 306;
Best Local Similarity	77.1%	Pred. No. 2.3e-29;		
Matches 185;	Conservative	0;	Mismatches 54;	Indels 1;
Gaps 1;				
QY	1168	GTAGAACAGTGAGAGAACCTAGAGTTGTAGTTTCAGACAACCACTGACATTGATATCTTG	1227	
Db	35	GTAACCAATCGTAGCCCTCGTGTGTGTGTAACAACCTGTAGTAGAGTTGATATCTTG	94	
QY	1228	ATGATGGCTATAGTGGAGAAATACGGGCAGAAAGTAGTGAAGGGCAATCCAAATCCAA	1287	
Db	95	ACGATGGGTATCGTTGGGCAATATATGGCAGAAAGTAGTGAAGGAAATCCCAACCCAC	154	
QY	1288	GGAGTTACTAAGTGACACACACCCAGGATGTCAGTAGGAGACGCTGGGAAGAGCCT	1347	
Db	155	GGAGTTACTAAGTGACACAAATACAGGATGCCCGTCAGGAAGCATGTTTGAGAGACAT	214	
QY	1348	CACATGACCTAAGGGCTGTGATCACAACTATGAGGGAAGCACACCACTATGTTCTCTG	1407	
Db	215	CACATGACCCGA-ATCGGTGATCACACATATGAGGAAACATACCATGATGCTCTG	273	

RESULT 2
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.

APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match 4.2%; Score 80.6; DB 1; Length 7218;
Best Local Similarity 4.3%; Pred. No. 6.4e-12;
Matches 14; Conservative 213; Mismatches 102; Indels 0; Gaps 0;
QY 8 TCTCATGGCATCTTCTTCTGTAGTTTGTAGACACCTCTGCAAGTGCAAACTCTTCACCAA 67
Db 1126 YY 1185
QY 68 CTTACCTCTCCACACACCTTCTATGACACCTTCTTCTGACCTCTGCTCTCTCC 127
Db 1186 YY 1245
QY 128 CTTGGACACACACAGCACCACACAGGTGTTCTGCTGAGAGACTGGCTCTGCTCTCC 187
Db 1246 YY 1305
QY 188 CAAATCAAGTCCACACACACCTCTCTGCTCTCTCTCCCTCTCCCTCTCTCTCTC 247
Db 1306 YY 1365
QY 248 TTCTACTTTGCTATCTCTCTGTTTGGCCCTGCTGAGCTTCTTCTGACTGCGCGTCT 307
Db 1366 YY 1425
QY 308 CCTTAACCTCTCCACACTTCTGCACTC 336
Db 1426 YYYYYYYYGTACCAAAATCTCTTCTATCTC 1454

RESULT 3

US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match 3.7%; Score 72.2; DB 1; Length 7218;
Best Local Similarity 4.3%; Pred. No. 1.3e-09;
Matches 17; Conservative 235; Mismatches 143; Indels 0; Gaps 0;
QY 1018 CAGAAACTCATCAATPACAAATTGGAGATGATGATTTGAGCAGAGTTCCCAAAAGTGA 1077
Db 1435 CRR 1376
QY 1078 AATCAGAGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1137
Db 1375 RRR 1316
QY 1138 GTGAAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197
Db 1315 RRR 1256
QY 1198 TTCAGACACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257
Db 1255 RRR 1196
QY 1258 AGAAGTAGTAGGAGCAATCCAAATCCAAAGGAGTTACTACAAGTGCACACCCAGGAT 1317
Db 1195 RRR 1136
QY 1318 GTCCAGTGAGGAGCAGGTGGAAGAGCCTCATGACCTAAGGGCTGTGATCACAACCT 1377

```

/ / TUBERCULOSIS
/ /
/ / TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
/ /
/ / NUMBER OF SEQUENCES: 350
/ /
/ / CORRESPONDENCE ADDRESS:
/ /   ADDRESSEE: SEED AND BERRY LLP
/ /   STREET: 6300 Columbia Center, 701 Fifth Avenue
/ /   CITY: Seattle
/ /   STATE: Washington
/ /   COUNTRY: USA
/ /
/ / ZIP: 98104-7092
/ / COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 329:
SEQUENCE CHARACTERISTICS:
LENGTH: 1105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-072-596-329

Query Match 2.3%; Score 45; DB 4; Length 1105;
Best Local Similarity 42.4%; Pred. No. 0.014;
Matches 108; Conservative 20; Mismatches 127; Indels 0; Gaps 0;
QY 1305 ACACACCCAGGATGTCAGTGAGGAGCAGCTGGAAAGACCTCACATGACCTTAAGGGCT 1364
DB 156 ACYTRACCCGCCAGYTCAGTGTTRAAACCGGTGYTRAGGCGCGACCAACWTAACGCT 215
QY 1365 GTGATCACAACCTTATGAGGAAAGACCAACCATGATGTTCTCGAGCCCGTGCAGTGGC 1424
DB 216 TTAACCAAGRAWYTGKTTGGTGGCCGCGACCCACCTGTTGTGGTCCCTCWTGCGGTGTAGC 275
QY 1425 AGCCATTCTGTGACAGACCAATGCCAAACAATGCTTCAAAACACACCAACACTCGAGCC 1484
DB 276 GCGGGTTANGCGCGGTGGCGGYTCAMCASCSCGCGGTATCCACKCNWTCGCCGCGC 335
QY 1485 ACTTCGGTAAGGCTTTGCCAGTGATCCACCAAGTGACAAATCCCTTCAGAACCAAGA 1544
DB 336 MRACCCACCGGCACTTTGACGGTGGCGCAATTCAAAYCKYKGTGRWTCCTCTCMAAACA 395
QY 1545 TCACAAGCACCA 1559
DB 396 CCACRAAGGCCACM 410

RESULT 7
US-09-328-352-112
Sequence 112, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 112
LENGTH: 1893
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-112

Query Match 2.3%; Score 43.8; DB 4; Length 1893;
Best Local Similarity 57.8%; Pred. No. 0.04; Mismatches 57; Indels 0; Gaps 0;
Matches 78; Conservative 0;
QY 1089 GATCAATATCATGAAGATGAACCTGATGCCAAAGATGGAATAATTGAAGGTGAAATGAG 1148

DB 235 GATGAAGTTGCTGAAGAAGAGCTCTGCCGCTGCTGTCATCTGTTGAAAATGAGCCTGA 294
QY 1149 GGTATGTCTAGCCCTGGAGTAGAACAGTGAAGAACCTTAGAGTTGTAGTTTCAGACAAAC 1208
DB 295 CGTAGCAGACCCCTGTACGTATGTACATGCGTGAATGGGTACAGTAGAAGTGTTRACC 354
QY 1209 ACTGACATTGTATC 1223
DB 355 CGTGAAGGTGAATC 369

RESULT 8
US-08-916-421B-1/c
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (191989)..(191989)

RESULT 9
 US-08-781-891-209
 ; Sequence 209, Application US/08781891
 ; Patent No. 6090620
 ; GENERAL INFORMATION:
 ; APPLICANT: Fu, Ying-Hui
 ; APPLICANT: Yu, Chang-En
 ; APPLICANT: Oshima, Junko
 ; APPLICANT: Mulligan, John T.
 ; APPLICANT: Schellenberg, Gerald D.
 ; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
 ; TITLE OF INVENTION: WERNER'S SYNDROME


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; OTHER INFORMATION: n equals a, t, c, or g
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; OTHER INFORMATION: n equals a, t, c, or g
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; OTHER INFORMATION: n equals a, t, c, or g

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US-08-916-421B-1

Query Match 2.0%; Score 39; DB 4; Length 1664976;
 Best Local Similarity 51.6%; Pred. No. 25;

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	Query Match	22.7%;	Score 437.2;	DB 9;	Length 2008;
	Best Local Similarity	57.4%;	Pred. No. 6.1e-114;		
	Matches 1000;	Conservative 0;	Mismatches 673;	Indels 69;	Gaps 9;
QY	17	ATCTCTCTCTGGTAGTTTAGACACCTCTCAAGTCGAAACTCTCTCACCACACTTCACCTT	76		
Db	23	ATCTCTCTCTCTATATGAGTTTTCATCTCTCTCAGGTATCACCTTGTGAACACACCCCTC	82		
QY	77	CTCCACACACCCCTTTTCATGACCACACTCTTTCTCTGTGACCTCTCTTCTCTCTCTCTTGACAA	136		

61 TCACCAACTTCACTTCTCCACACACCCCTTTCATGACCACTTCTTCTCTGACCTCCTTG 120
Db
75 TCACCAACTTCACTTCTCCACACACCCCTTTCATGACCACTTCTTCTCTGACCTCCTTG 134
QY 121 CTTCTCCCTTGGACAAACAAGCCACCAAGGCTGTTGCTGAGAGAACTGGCTCTG 180
Db 135 CTTCTCCCTTGGACAAACAAGCCACCAAGGCTGTTGCTGAGAGAACTGGCTCTG 194
QY 181 GTGTTCCCAAAATTCAGTCCACACCACTTCTCTCTGCTCTCTCTCTCCCTCCCATTT 240
Db 195 GTGTTCCCAAAATTCAGTCCACACCACTTCTCTCTGCTCTCTCTCTCCCTCCCATTT 254
QY 241 CTCCTCTCTTCTTCTTCT 300
Db 255 CTCCTCTCTTCTTCTTCT 314
QY 301 CGGTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 359
Db 315 CGGTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 373
RESULT 3
US-09-878-574-4924
; Sequence 4924, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Thompson, Michael D.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 4924
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-001-Q1-B1-C9
US-09-878-574-4924
Query Match 17.7%; Score 342.2; DB 10; Length 421;
Best Local Similarity 93.2%; Pred. No. 3.5e-87;
Matches 372; Conservative 0; Mismatches 18; Indels 9; Gaps 1;
QY 4 CGAGTCTCATGGCATCTTCTTCTGTTAGTCTGACACCTCTGCAAGTGCAAACTCCTTCA 63
Db 23 CGGCTCGAGTGGCATCTTCTTCTGTTAGTCTGACACCTCTGCAAGTGCAAACTCCTTCA 82
QY 64 CCAACTTCACTTCTCCACACACCCCTTTCATGACCACTTCTTCTCTGACCTCCTTGCTT 123
Db 83 CCAACTTCACTTCTCCACACACCCCTTTCATGACCACTTCTTCTCTGACCTTCTTGCTT 142
QY 124 CTCCTTGGACAAACAAGCCACCA-----GGGTGGTGTGCTGAGAGAACTG 174
Db 143 CTCCTTGGACAAACAAGCCACCA-----GGGTGGTGTGCTGAGAGAACTG 202
QY 175 GCTCTGGTGTCCCAATTCAGTCCACACACCACTTCTCTGCTCTCTCTCTCCCTC 234
Db 203 GCTCTGGTGTCCCAATTCAGTCCACACCACTTCTCTGCTCTCTCTCTCTCTCTCTC 262
QY 235 CCAATTCCT 294
Db 263 CCAATTCCT 322
QY 295 ACTCGCGGTCTCTTAACTTCTTCAACATCTGCAATCTGCAATCTGCAATCTGCAATCT 354
Db 323 ACTCACCTGTCTCTTAACTTCTTCAACATCTGCAATCTGCAATCTGCAATCTGCAATCT 382
QY 355 TTGCTCAGAGCTTCAATTTGAAGAGAGAGTTCAGGGGGA 393

Db 383 TTGCTCGGAGCTTCAATTTGAAGAGAGAGTTCGGGGGGA 421
RESULT 4
US-09-878-574-1921
; Sequence 1921, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Thompson, Michael D.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1921
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-031-Q1-B1-C6
US-09-878-574-1921
Query Match 16.2%; Score 312.6; DB 10; Length 363;
Best Local Similarity 93.7%; Pred. No. 9.6e-79;
Matches 340; Conservative 0; Mismatches 14; Indels 9; Gaps 1;
QY 15 GCATCTTCTTCTGTTAGTCTGACACCTCTGCAAGTGCAAACTCCTTCAACCACTTCACC 74
Db 1 GCATCTTCTTCTGTTAGTCTGACACCTCTGCAAGTGCAAACTCCTTCAACCACTTCACC 60
QY 75 TTCTCCACACACCTTTCATGACCACTTCTTCTCTGACCTCTCTGCTCTCTGCTCTGCTG 134
Db 61 TTCTCCACACACCTTTCATGACCACTTCTTCTCTGACCTCTCTGCTCTCTGCTCTGCTG 120
QY 135 AACCAACAGCCACCA-----GGGTGGTGTGCTGAGAGAACTGGCTCTGCTGTT 185
Db 121 AACCAACAGCCACCA-----GGGTGGTGTGCTGAGAGAACTGGCTCTGCTGTT 180
QY 186 CCAAAATTCAGTCCACACCACTTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 245
Db 181 CCAAAATTCAGTCCACACCACTTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 246 TCT 305
Db 241 TCT 300
QY 306 CTCCTTAACTTCCAAACATCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCTGCA 365
Db 301 CTCCTTAACTTCCAAACATCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCTGCA 360
QY 366 TTC 368
Db 361 TTC 363
RESULT 5
US-09-938-842A-804
; Sequence 804, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A

Db 1178 CGACGGTTACAGATGGAGAAATACGCCAGAAAGTCGTTAAGGGAAACCCAAATCAAAG 1237
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 QY 1349 ACATGACCTTAAGGGCTGTGATCAACAATTATAGGGAAAGCAACACATGATGTTCTCTGC 1408
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 QY 1409 AGCCCGTGGCAGTGG 1423
 Db 1358 AGTCGTGGTAGCGG 1372

RESULT 7
 US-10-278-173-87
 ; Sequence 87, Application US/10278173
 ; Publication No. US20030061637A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Cai-Zhong
 ; APPLICANT: Broun, Pierre
 ; APPLICANT: Riechmann, Jose-Luis
 ; APPLICANT: Pineda, Omaira
 ; APPLICANT: Zhang, James
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Pilgrim, Marsha
 ; APPLICANT: Keddle, James
 ; APPLICANT: Heard, Jacqueline
 ; APPLICANT: Reuber, Lynne
 ; APPLICANT: Ratcliffe, Oliver
 ; APPLICANT: Adam, Luc
 ; APPLICANT: Samaha, Raymond
 ; TITLE OF INVENTION: POLYNUCLEOTIDES FOR ROOT TRAIT ALTERATION
 ; FILE REFERENCE: MEI-009
 ; CURRENT APPLICATION NUMBER: US/10/278,173
 ; PRIOR FILING DATE: 2002-10-21
 ; PRIOR APPLICATION NUMBER: US/09/533,392
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 60/125,814
 ; PRIOR FILING DATE: 1999-03-23
 ; NUMBER OF SEQ ID NOS: 177
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 87
 ; LENGTH: 1398
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; OTHER INFORMATION: G177
 US-10-278-173-87

Query Match 14.0%; Score 270.6; DB 15; Length 1398;
 Best Local Similarity 62.5%; Pred. No. 2.7e-66;
 Matches 473; Conservative 0; Mismatches 254; Indels 30; Gaps 2;
 QY 683 ACAATCTCAGACTTTAAGTAGAAGGTCCAGATGATGGTACAAATGGAGAAATATGGCCA 742
 Db 538 ACCAGCATACATGTTGAGTAGGACTCTAATGATGTTATGTTGGAGAAATACGGTCA 597
 QY 743 AAAACAAGTGAAGGGAAGTGAATAATCAAGAAGTTATTAACAATGCATATACCCCAATTG 802
 Db 598 GAAACAAGTGAAGGGAAGGGAACCCCTAGGAGTTACTTCAAGTGATCGTATCCTGATTG 657
 QY 803 CCTTACAAAGAGAGGTTGAGAGGTCCTTAGTGGACAAATTAAGTATGATGTTATATAA 862
 Db 658 TGTTCCTCAAGAGATGTTGAGAGGCTCTGATGGACAGATCACTGATCATTTTATAA 717
 QY 863 GGGTACTCAATCAATCCCTAAGCCTCAAAATACCTAGGAGAACTCATCAAACTCCTCTTC 922
 Db 718 AGTGTGTCATATCATCTTAAGCCTGAGTTCACCAAGAGA----- 757
 QY 923 TCTTGAATCCCTCAATTCATTAATTCATGAACTGAAATCCAGATCAATCCTATGCCAC 982

Db 758 -----CCATCTCAATCTTCATTCACATCATCGGTTAATGGAGGCGCTTGTTTAATCC-- 810
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 Db 811 ---TGCCTCTGTTGTAGTGAACCTCATGATCAATCAGAGAACTCTTCGATTCGTTTGA 867
 QY 1043 AGATGATGATTTTGAAGAGAGTTCACAAAAGTGTAAATCAGAGGGGATGAATATGATGA 1102
 Db 868 CTATAGTATCTTTGAGCAGAAAAAGTTTTAAATCAGAGTATCGTGAGATAGATGAAGAGA 927
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RESULT 8
 US-09-938-842A-1681
 ; Sequence 1681, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1681
 ; LENGTH: 1182
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1681

Query Match 14.0%; Score 270.2; DB 10; Length 1182;
 Best Local Similarity 63.3%; Pred. No. 3.1e-66;
 Matches 463; Conservative 0; Mismatches 238; Indels 30; Gaps 2;
 QY 683 ACAATCTCAGACTTTAAGTAGAAGGTCCAGATGATGGTACAAATGGAGAAATATGGCCA 742
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 QY 923 TCTTGAATCCCTCATTAATTTCCATCAGAACTGAAATCCCGAGATCAATCTATGCCAC 982
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 Db 798 CTATAGTGATCTTGAGCAGAAAGATTTTAAATCAGAGTATGGTGAGATAGTGAAGAGA 857
 QY 1103 AGATGAACCTGATGCCAAAGAGTGAATAATGAAGTGAATAATGAGGGTATGTCAGCCCC 1162
 Db 858 GGAACAACCTGAGATGAAGAGGATGAAGAGAGGATGAAGATGAAGAGGATGCTATAGA 917
 QY 1163 TCGAAGTAGACAGTGAAGAACTAGAGTTGATGTTTACAGAACACCAAGTGCATTCAT 1222
 Db 918 AGTAAGCAAGAGGATTAAGAGGCAAGAGTTGTGTTTCAACAAATGATGATGATGAT 977
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 Db 1098 ATCCGACGACAGAGAGAGAGGATTTCTCACTTACCTATGAAGGAAGACACAAATCAGAT 1157
 QY 1403 TCTGACAGCCC 1413
 Db 1158 CCCAACGGCG 1168

RESULT 9
 US-09-878-574-8719
 ; Sequence 8719, Application US/09878574
 ; Patent No. US20020110548A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Byrum, Joseph R.
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Thompson, Michael D.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(15401)B
 ; CURRENT APPLICATION NUMBER: US/09/878,574
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 09/333,535
 ; PRIOR FILING DATE: 1999-06-14
 ; NUMBER OF SEQ ID NOS: 15775
 ; SEQ ID NO 8719
 ; LENGTH: 265
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; OTHER INFORMATION: Clone ID: 701101569H1
 US-09-878-574-8719

Query Match 13.3%; Score 256; DB 10; Length 265;
 Best Local Similarity 98.1%; Pred. No. 1.3e-62;
 Matches 259; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 510 ACACAAAGCCATGAGGTTTTCAGAGGCCAGAAAACAGGATAATTTTTCTCAGAAAG 569
 Db 2 ACACAAAGCCATGAGGTTTTCAGAGGCCAGAAAACAGGATAATTTTTCTCAGAAAG 61
 QY 570 GGTATGATGAAAACCTGAAAACCTCTTCTCCATGAGAGTTTTCCCTGAGATTCCTAGT 629
 Db 62 GGTATGATGAAAACCTGAAAACCTCTTCTCCATGAGAGTTTTCCCTGAGATTCCTAGT 121
 QY 630 GTCCAAAACCTAACCATAGCAATGGGTTTCAATCCGATTTATGGCAATTTACCCCCCAATCT 689
 Db 122 GTCCAAAACCTAACCATAGCAATGGGTTTCAATCCGATTTATGGCAATTTACCCCCCAATCT 181
 QY 690 CAGACTTTAAGTAGAAGTGCAGATGATGGGTACAAATGGAGGAAATATGGCCAAAACAA 749
 Db 182 CAGACTTTAAGTAGAAGTGCAGATGATGGGTACAAATGGAGGAAATATGGTCAAAACCCA 241
 QY 750 GTGAAGGGAAGTGAATAATCCAAGA 773
 Db 242 GTGAAGGGAAGTGAATAATCCAAGA 265

RESULT 10
 US-10-341-961A-18
 ; Sequence 18, Application US/10341961A
 ; Publication No. US20040006787A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.
 ; APPLICANT: Curagen Corporation
 ; APPLICANT: Crasta, Oswald
 ; APPLICANT: Swirsky, Peter
 ; APPLICANT: Mysore, Kiran
 ; APPLICANT: Folkerts, Otto
 ; APPLICANT: Martin, Gregory
 ; APPLICANT: Ekegren, Sophia
 ; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGE
 ; FILE REFERENCE: BTI.67A2
 ; CURRENT APPLICATION NUMBER: US/10/341,961A
 ; PRIOR FILING DATE: 2003-01-14
 ; PRIOR APPLICATION NUMBER: 60390249
 ; PRIOR FILING DATE: 2002-06-20
 ; PRIOR APPLICATION NUMBER: 60261029
 ; PRIOR FILING DATE: 2001-01-11
 ; PRIOR APPLICATION NUMBER: 60348792
 ; PRIOR FILING DATE: 2002-01-14
 ; NUMBER OF SEQ ID NOS: 395
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 496
 ; TYPE: DNA
 ; ORGANISM: Lycopersicon esculentum
 US-10-341-961A-18

Query Match 12.1%; Score 232.8; DB 12; Length 496;
 Best Local Similarity 71.3%; Pred. No. 8.9e-56;
 Matches 338; Conservative 0; Mismatches 127; Indels 9; Gaps 2;
 QY 911 AAATCTCTCTCTTCTTGGCAATCCCTCATTCATAATCCATCAGAACTGAAATCCAGATCA 970
 Db 32 AGATCATCTTCAATCATGATTTCAAAACCTTGTCTTACTCAACTGATGATGATGATGATGAT 91
 QY 971 ATCTATGCGACACATGGAAGTGCACAAATGGATTGAGTTCAGCTGCCACCCAGAAATCATC 1030
 Db 92 GCCAAACGGGTTCTTGAATAATGGTCAAGAGACTCTTTGCTGTGTACAGACAAATCTTC 151
 QY 1031 AATATCAATGGAGATGATGATTTTGAAGCAGAGTTCCTCCAAAAGTGTAAATCAGAGGGGA 1090
 Db 152 AGCTTCTTTTGGAGATGAGATGTTGATCAAGGCTCTCTCTATCAGTAAATCAGGA----- 206
 QY 1091 TGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1150
 Db 207 -GAAATGATGATAATGAAACCCCGAGCAAGAGATGGAAGGTTGACATGGAATGGAACGAGGT 265

QY 1151 TATGTCAGCCCCCTGGAAGTAGAACAAGTACAGAGAACCTAGAGTTGTAGTTGACAGAACCAAG 1210
 Db 266 TATATCA---TCTGCAAGTAGAACAAGTACAGAGAACCTAGAGTTGTAGTTGACAGAACCAAG 322
 QY 1211 TGACATTGATATCTTTGATGATGGCTATAGGTGGAGAAATACGGCAGAAAGTACTGAA 1270
 Db 323 TGACATTGATATCTTTGATGATGGCTATAGGTGGAGAAATACGGCAGAAAGTACTGAA 382
 QY 1271 GGGCAATCCAAATCCAAAGAGTTACTACAAAGTGCACACACCCAGGATGTCCAGTGAAGAA 1330
 Db 383 AGGAATCCAAACCCAGAGTTACTACAAAGTGCACATTTACTGGATGTCCGGTTAGAA 442
 QY 1331 GCACGTGGAAGAGCTTCATGACCTAAGAGGCTGTGATCACAACCTATGAGGG 1384
 Db 443 GCATGTGGAACGAGCATCTCATGATCTAAGAGCGGTTATCACAACCTATGAGGG 496

RESULT 11
 US-09-810-264-23
 ; Sequence 23, Application US/09810264
 ; Patent No. US2002007675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Crane, Virginia C.
 ; APPLICANT: Hu, Xu
 ; APPLICANT: Lu, Guihua
 ; APPLICANT: Zhang, Lingyu
 ; TITLE OF INVENTION: WRKY Transcription Factors and Methods
 ; FILE REFERENCE: 1183
 ; CURRENT APPLICATION NUMBER: US/09/810, 264
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: US 60/190,467
 ; PRIOR FILING DATE: 2000-03-17
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 23
 ; LENGTH: 2343
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 US-09-810-264-23

Query Match 12.1%; Score 232.8; DB 9; Length 2343;
 Best Local Similarity 59.5%; Pred. No. 2.6e-55;
 Matches 437; Conservative 0; Mismatches 282; Indels 15; Gaps 2;

QY 703 GAAGTCAGATGATGGGTACAAATGGAGGAATATGCGCCAAACAAAGTGAAGGAGTG 762
 Db 867 GAGTATCTGATGATGATACAACTGGAGAAATATGGCAAAACATGTTAAAGGAAGTG 926
 QY 763 AAAATCCAAAGAGCTTATCAAAATGCACATACCCCAATTCGCCCTACAAAGAAAGGTTG 822
 Db 927 AATTTCCAGCAGTTATACAAATGACATCCTAATCTGTGAAGTTAAGAACTATTGTG 986
 QY 823 AGAGGTCTTTAGTAGGACAAATTTACTGAGATAGTTTATAAGGGTACTCATACCATCTTA 882
 Db 987 AAGCTCCCATGATGACAAATCACTGAGATATTTTACAAGGGAACACATGATCATCTTA 1046
 QY 883 AGCTCAAAATACCTAGAGAACTCATCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 942
 Db 1047 AACCTCAACCAACCCCGGTTACTCTGCAGGAACCTATAATGTCTGTGCAAGAGACAGAT 1106
 QY 943 ATTCCATCAGAACTGAATCCAGATCAATCTCTATGCCACATGGAAGTGGCAAAATG- 1001
 Db 1107 CTGATAAGCTTTTGTACTAGCCGAGATGACAAAGATCCAAATATGTGTGGCCAGGGT 1166
 QY 1002 -----GATTCAGTGTCCACCCAGAAACCTCATCAATATCAATTTGGAGATGATG 1050
 Db 1167 CTCACCTGGCTAGCCGAGCGGTAAACAGAGTTATTTGCTGTAGCAACAATGATGGTG 1226
 QY 1051 ATTTGAGCAGAGTTCCCAAAAGTGAATCAGAGGGGAGTGAATATGATGAAGTGAAC 1110
 Db 1227 ATCTAGATGTTTGGGGGTTTGTCAACCGGAATATGATGATGATGATGATGATGATGATC 1286

QY 1111 CTGATGCCAAAGAGATGGAATTTGAAGGTGAAATAGGGGTATGTGAGCCCTCGGAAGTA 1170
 Db 1287 CTTTCTCTCAAGCGAAGAAATATGGACGTTTGGAAATTTGCTGACAT---CACTCTCTGATTTA 1343
 QY 1171 GAACAGTGAAGAACCTAGAGTTGTAGTTTCAGAACACAGTGCACATTTGATATCTTGTATG 1230
 Db 1344 ACCTTATCCGGGAGCCACGTTGTTGTGTACAAACTCTGAGTGAGGTTGATATCTTGGATG 1403
 QY 1231 ATGGCTATAGGTGGAGAAATACGGGCAGAAATAGTGAAGGCAATCCAAATCCAAAGTA 1290
 Db 1404 ATGGCTATCGCTGGCGCAAGTATGGCGAAGGTGTGAGGCAATCTTAACCTTAGA 1463
 QY 1291 GTTACTACAAGTGCACACCCAGGATGTCCAGTGAAGGACACGTTGGAAGAGGCTCAC 1350
 Db 1464 GTTATTACAATGCAGAACACCGGTTGCCCGGTTAGAAAAACACGTTGAGAGGGCATCTC 1523
 QY 1351 ATGACCTAAGGCTGTGATCACAACCTATGAGGGAAGACCAACCATGATGTTCTGCGAG 1410
 Db 1524 ATGATCCAAAGCTGTGATTTACAGTATGAGGGGAAACACAATCATGATGTACCAACTG 1583
 QY 1411 CCCGTGGCAGTGGC 1424
 Db 1584 CAAGGAATAGTTGC 1597

RESULT 12
 US-10-341-961A-156
 ; Sequence 156, Application US/10341961A
 ; Publication No. US20040006787A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.
 ; APPLICANT: Curagen Corporation
 ; APPLICANT: Crasta, Oswald
 ; APPLICANT: Swirsky, Peter
 ; APPLICANT: Mysore, Kiran
 ; APPLICANT: Folkerts, Otto
 ; APPLICANT: Martin, Gregory
 ; APPLICANT: Ekengren, Sophia
 ; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGE
 ; FILE REFERENCE: BTI.67A2
 ; CURRENT APPLICATION NUMBER: US/10/341,961A
 ; CURRENT FILING DATE: 2003-01-14
 ; PRIOR APPLICATION NUMBER: 60390249
 ; PRIOR FILING DATE: 2002-06-20
 ; PRIOR APPLICATION NUMBER: 60261029
 ; PRIOR FILING DATE: 2001-01-11
 ; PRIOR APPLICATION NUMBER: 60348792
 ; PRIOR FILING DATE: 2002-01-14
 ; NUMBER OF SEQ ID NOS: 395
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 156
 ; LENGTH: 574
 ; TYPE: DNA
 ; ORGANISM: Lycopersicon esculentum
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (530)..(530)
 ; OTHER INFORMATION: Unknown nucleotide 530
 US-10-341-961A-156

Query Match 11.9%; Score 229.2; DB 12; Length 574;
 Best Local Similarity 68.4%; Pred. No. 1.1e-54;
 Matches 347; Conservative 0; Mismatches 154; Indels 6; Gaps 2;

QY 638 TAACCATAGCAATGGGTTTCAATCCGATTATCGCAATTACCCCCCACAATCTCAGACTTT 697
 Db 71 TATGCGAGATATATATGATGATGACAAATAGTGTGAAACCAATACATACAGATATAGGGA 130
 QY 698 AAGTGAAGGTGAGATGATGGGTACAAATTTGGAGGAATATGCGCAAAACAAGTGAAGGG 757
 Db 131 GCAGAAAAGGTGAGATGACGGGATACAAATTTGGAGGAATACTGCTGAAAACAAGTAAAGG 190

QY 758 AAGTGAATCCAGAGGTTATTACAAATGCATACCCCAATTGCGCTACAAAGAGAA 817
DB 191 TAGTGAAATCCGAGAGGCTACTACAAGTGATCATACCCCAATTGTCCACCATGAGAA 250
QY 818 GGTGAGAGGCTCTTTAGATGGACAAATTAAGTATGAGATAGTTTATAAGGGTACTCATAACCA 877
DB 251 GGTGAGAGATCTTTAGATGGTCAAAATTAAGTATGAGATAGTTTATAAGGGTACTCATAACCA 310
QY 878 TCTAAGGCTCAAAATTAAGTATGAGATAGTTTATAAGGGTACTCATAACCA 937
DB 311 TCCAAAGGCTCAGTACCAAGAGATCGTCATCATCCAGAGCTTCTATCTGCAATCCAAATC 370
QY 938 TCCAAATTCATCAGAACTCAATCCAGATCAATCCATGATCCACATGGAAGTGGACA 997
DB 371 TTAACAATACAAATTAAGTATGAGATAGTTTATAAGGGTACTCATAACCA 427
QY 998 AATGGATTCAGTGGCCACCCAGAAATCAATCAATATCAATTTGGAGATGATGATTTGA 1057
DB 428 AATGGATTCGTTGCAACACCTGAGATCTTCTGATTTCAATTTGGGATGATGATCA 487
QY 1058 GCAGAGTCCCAAG---TGTAATCAGAGGGGATGAATATGATGAAGTGAACCTGA 1114
DB 488 ACACACTTGTCAAAAGAGTAGTAGTCAAGAGAGATGATCTGATGAAGAGGAACCA 547
QY 1115 TGCCAAAGATGAAATTCAGGTGA 1141
DB 548 CTCATAAGATGAAAGAGAAACGA 574

RESULT 13

US-09-938-842A-425
; Sequence 425, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Kreps, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 425
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-425

Query Match 11.9%; Score 228.8; DB 10; Length 1542;
Best Local Similarity 58.9%; Pred. No. 2.8e-54;
Matches 442; Conservative 0; Mismatches 287; Indels 21; Gaps 2;
QY 682 CACATCTCAGACTTTAAGTAGAGGTTCAGATGATGGTCAATTTGAGGAGGAAATATGGCC 741
DB 719 CACAGCTCAAAATGCTGACAAACCAAGCTGATGATGATCAACTGCGGGAATATGGC 778
QY 742 AAAAACAAGTGAAGGGAAGTGAATTCACAAAGTATTACAAATGCATATACCCCAATT 801
DB 779 AGAAGCAAGTGAAGGAGGCGGATTTCTCGAGTTATTACAAATGTACCAATCCAGCTT 838
QY 802 GCCCTCAAAAGAGAGGTTGAGAGGTTCTTTAGATGAGCAAAATTAAGTATGATTTATA 861
DB 839 GTCCTGTCAAGAGAGAGAGGAGGTCCTCGATGAGCAAGTAAACGGAATATCATCTACA 898

QY 862 AGGTACTCTAATCAACCATCTAAGCCTCAAAATATCTAGGAGAAATCTCATCAAACTCTCTT 921
DB 899 AGGTCAACCAACATCATGAGCTTCTCAAAAGCGGGTAAACAAATCAACGGGAGTTGTAAAA 958
QY 922 CTCCTTGCATCCCTCATTCAAATTCATCAGAACTGAAATCCAGATCAATCCTATGCCA 981
DB 959 GTTCTGATATTGCAAAATCAGTTTCAAAACAGTAATAGCAGTCTCAACAGAGTAAGGG 1018
QY 982 CACATGGAAGTGCACAAATGGATTTCAGCTGCCACCCAGAAATCTCATCAATATCAATTTG 1041
DB 1019 ACCAGAAACAGCCA-----AGTTCAACAAACAGAGCAGATGCTGAAGCAGTG 1069
QY 1042 GAGATGATGATTTGAGCAGAGATTCACCAAGTGTAAATCAGAGGGGATGAATATGATG 1101
DB 1070 ATAGCGAGGAGGTTGG-----AATGCAGAGACTAGTGTGGGAGAAAGACATG 1117
QY 1102 AAGATGAACCTGATGCCAAAGATGGAATTTGAAGTTGAAATGAGGTGAAATGAGGTATGTCAGCCC 1161
DB 1118 AGGATGAGCTGATCCCAAGCGAAGAAATACAGAAAGTTTCGGGTTTCAGAAACCAAGTTGCTT 1177
QY 1162 CTGGAAGTAGAACAGTGTAGAGAACCTAGAGTTGTAGTTTTCAGACAAACCAAGTGAATGATA 1221
DB 1178 CATCGATAGAACTGTGACAGAGCTTAGGATTTATGTCAAACGAGAGTGAAGTTGACC 1237
QY 1222 TCTTTGATGATGGCTATAGTGGAGAAATACGGCAGAAAGTGTGAAGGGCAATCCAA 1281
DB 1238 TCTTAGATGATGATAGTGGCGCAAGTATGTCAGAAAGTGTGCAAAAGGAAATTCCTT 1297
QY 1282 ATCCAGAGGTTACTACAGTGCACACACCCAGGATGTCAGTGGAGGACGCTGGAAA 1341
DB 1298 ATCCGAGGAGTACTATTAAGTGTACAAACCAAGTTTCGGAGTAAAGGAAACATGTAGAGA 1357
QY 1342 GAGCCTCACATGACCTTAAGGGCTGTGATCACAATTTATGAGGAAAGACCAACCATGATG 1401
DB 1358 GAGCAGCAACTACCCAAAGCTGTGTAACAACATATGAGGTAAGGAAACATATACCATGATG 1417
QY 1402 TTCTGTCAGCCGCTGGCAGTGGCAGCCATT 1431
DB 1418 TTCCAGCTCTAGAACCCAGCAGCCATCACT 1447

RESULT 14

US-10-295-403-77
; Sequence 77, Application US/10295403
; Publication No. US20030101481A1
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc
; APPLICANT: Broun, Pierre
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, Lynne
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Keddle, James
; APPLICANT: Zhang, James
; APPLICANT: Benito, Maria-Ines
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fromm, Mike
; TITLE OF INVENTION: PLANT GENE SEQUENCES I
; FILE REFERENCE: MBI-0003
; CURRENT APPLICATION NUMBER: US/10/295,403
; PRIOR FILING DATE: 2002-11-15
; PRIOR FILING DATE: 1999-09-13
; PRIOR FILING DATE: 1999-09-13
; PRIOR FILING DATE: 1999-09-13
; PRIOR FILING DATE: 1998-09-22
; PRIOR FILING DATE: 1998-10-06
; PRIOR FILING DATE: 1998-10-06
; PRIOR FILING DATE: 1998-11-17
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 170

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 77

; LENGTH: 2044

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (197)..(1735)

; OTHER INFORMATION: G878

; OTHER INFORMATION: "n" at various positions throughout the sequence

; OTHER INFORMATION: may be A, T, C, G, other or unknown

US-10-295-403-77

Query Match 11.9%; Score 228.8; DB 15; Length 2044;

Best Local Similarity 58.9%; Pred. No. 3.4e-54;

Matches 442; Conservative 0; Mismatches 287; Indels 21; Gaps 2;

QY 682 CACAACTCTCAGACTTTAAGTAGAAGTTCAGATGCGGTCAATTTGAGGAAATATGGCC 741

Db 915 CACAGCCTCAAAATGCTGACAAACCACTGATGATGATGATGATGATGATGATGATG 974

QY 742 AAAAACAAGTGAAGGGAAGTGAATCCAAAGAGTTATTACAAATGCACATACCCCAATT 801

Db 975 AGAAGCAAGTGAAGGGAAGGAGTTTCTCGAGTTATTACAAATGATGATGATGATGATG 1034

QY 802 GCCTTCAAAAGAAAGGTTGAGAGGTCTTTAGATGACAAATTTACTTGATAGTTTATA 861

Db 1035 GTCTGTGCAAGAAAGTGAAGGTCACCTCGATGACAAAGTAAACGGAATCATCTACA 1094

QY 862 AGGTACTATACCATCTTAAGCCTCAAAATCTAGGAGAAATCATCAAACTCCTCTT 921

Db 1095 AGGTCAACAATCATGAGCTTCTCAAAAGCGCGTTAACAATAACGGGAGTTGAAAA 1154

QY 922 CTCTTGCAATCCCTCATTTCAATTCATCAGAACTGAAATCCCAGATCAATCTATGCCA 981

Db 1155 GTCTGATATTGCAATTCAGTTTCAAAAGTAATAGCAGTCTCAACAGAGTAAGAGGG 1214

QY 982 CACATGGAAGTGAACAAATGGATTCACTGCCACCCAGAAATCTCATCAATATCAATTG 1041

Db 1215 ACCAGGAAACAAGCA-----AGTTACAAACACAGAGCAGATCTCTGAAGCAAGTG 1265

QY 1042 GAGATGATATTTAGCAGAGTTCCTCAAAAGTGTAAATCAGGAGGGAATGAATATGATG 1101

Db 1266 ATAGCGAGGAGGTTGGG-----AATGACAGAGACTAGTGTGGGAGAAAGACATG 1313

QY 1102 AAGTGAACCTGATGCCAAAGATGGAATTTGAAGTGAATGAGGTATGATGATGATGATG 1161

Db 1314 AGGATGACCTGATGCCAAAGCAAGTAATACAGAAAGTTGCGGTTTCAGAACCAAGTTGCTT 1373

QY 1162 CTGGAAGTAGAACAAGTGAAGAACCTAGAGTTGTAGTTTCAGACAAACAGTGAATGTATA 1221

Db 1374 CATCGCATAGAACTGTGACAGAGCTAGGATTTATGTTCAAAACGACGATGAAGTTGACC 1433

QY 1222 TCCTTGATGATGCTATAGTGTGAGAAATACCGGCAAGAAAGTAGTGAAGGGCAATCCAA 1281

Db 1434 TCTTAGATGATGATA TAGGTGGCGCAAGTATGCTCAGAAAGTAGTCAAAAGGAAATCCTT 1493

QY 1282 ATCCAGAGGTACTACAAAGTGCACACCCAGGATGTCAGTGAAGAACGACGTGGAAA 1341

Db 1494 ATCCAGAGGACTACTATAGTGTACACACCAAGATTGCGGAGTAGGAAACATGTATAGA 1553

QY 1342 GAGCCTCACATGACCTAAGGCTGTGATCACACTTATAGGGAAGACCAACCATGATG 1401

Db 1554 GAGCAGCACTGACCCAAAGCTGTGTATCAACATATAGAGTAACATCAATCAATGATG 1613

QY 1402 TTCCTGAGCCCGTGGCAGTGGCAGCCATT 1431

Db 1614 TTCAGCTGCTAGAACCAAGCAGCAGCCATCAGT 1643

RESULT 15

US-09-938-842A-2279

; Sequence 2279, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE OF INVENTION: SAME, AND METHODS OF USE

; FILE REFERENCE: SCRIPT1300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 2279

; LENGTH: 1545

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-2279

Query Match 11.5%; Score 221.4; DB 10; Length 1545;

Best Local Similarity 59.0%; Pred. No. 3.7e-52;

Matches 447; Conservative 0; Mismatches 286; Indels 24; Gaps 3;

QY 679 CCCCAATCTCAGACTTTAAGTAGAGTTCAGATGCGGTACATTTGAGGAAATATG 738

Db 653 CCAACAGCCTCTAAATGTTGCAAAACCACTGATGATGCTATACTGCGGAAATATG 712

QY 739 GCCAAACAAGTGAAGGGAAGTGAATCCAAAGAGTTATTACAAATGCACATACCCCA 798

Db 713 GCGAAAGCAGTTAAGTAGGAGTTCCAGAGCTATTACAACTGTACTTAATCCAG 772

QY 799 ATTGCCCTCAAGAAGAGGTTGAGAGTCTTTAGATGCAAAATTAATGAGATAGTTT 858

Db 773 GATGCTCTCAAGAAGAGGTTGAGAGTCTCTTGATGCAAGTAAACGAGATTATCT 832

QY 859 ATAAGGTACTATTAACCATCTTAAGCCTCAAAATTAAGTAGGAGAACTCATCAACTCT 918

Db 833 ACAAAGGTGAGCAGCAATCATGAACCTCTCTCAAAACACTAAGCGAGGTAAACAAAGATAA 892

QY 919 CTCTCTTCCCAATCCCTCAATCAAA-----ATTCCATCAGAACTCAAAAT 961

Db 893 CCGGAAATTAATGAGGAGTTGATTAATAACATCCGCGGAGTTCTGATTTGGGGGAT 952

QY 962 CCCAGATCAATCCTA-----TGCCACACATGGAAGTGGACAAATGGATTTCAGCTGCCACCC 1017

Db 953 CACAGTTTCAAACTAATAGCTCCAAACAGACTTAAGAGAGAGCAACATGAAGCAGTAAGTC 1012

QY 1018 CAGAAACTCATCAATATCAATTTGAGAGTATGATTTTGAAGCAGAGTTCCTCAAAAGTGA 1077

Db 1013 AAGTACGACAAACAGAGCACTTTGCTGAGGCAAGTGCAGCTGAAGAAAGTTGGTAAATGGAG 1072

QY 1078 AATCAGGAGGAGTGAATATGATGATGAATGAACCTGATGCAAAAGATGCAAAATGAAG 1137

Db 1073 AAATGATGTGAGAGAGAAAGATGAGATGAGCTGATCCCAAGAGAAAGTACAGAAG 1132

QY 1138 GTGAAAT---GAGGATATGTCAGGCCCTTGGAAAGTAGAACAGTGAGAGAACCTTAGAGTTG 1194

Db 1133 TTCCGATTTCAAGAACCACTCTGCTGCTTTCATATAGAACTGTGACAGAGCTTAGAATTA 1192

QY 1195 TAGTTTCAGACAAACAGTGCATGATATCTTTGATGATGCTGCTATAGGTGAGAGAAATAGC 1254

Db 1193 TTGTCCAAACGACGAGTGAAGTTGATCTTCTAGATGATGGATATAGGTGGCGTAAATATG 1252

QY 1255 GCGAGAAAGTGTGAGGCGCAATCCAAATCCAGGAGTTACTACAGTGCACACACCCAG 1314

Db 1253 GACAGAAAGTTGTCAAAAGGGAATCCTTTATCCGAGGAGCTACTACAAAGTGCACACACCCAG 1312

QY 1315 GATGTCCAGTGAGGAGCAGCGTGGAAAGAGCCTCATGACCTTAAGGGTGTGATCACAA 1374

Db 1313 GATGTGTGTGAGGAACATGTTAGAGAGAGACCAACAGATCCAAAAGCTGTAGTAACAA 1372
Qy 1375 CTTATGAGGGAAGCAACCATGATGTTCTTCGAGC 1411
Db 1373 CATATGAAGGAAACATAACCATGACCTTCCCGCTGC 1409

Search completed: January 20, 2004, 21:28:58
Job time : 649 secs